

Alignment 1

Figure 1

Page 1

[illegible]

	10	20	30	40	
1	A G A G T T T G A T C C T G G C T C A G	A C G A A C G C T G G C G G C G T G C	43030	16S	
1	- - - - - - - - - - - - - - - - -	G A C G A A C G C T G G C G G C G T G C	49025	16S	
1	A G A G T T T G A T C C C T G G C C T C A G	G A C G A A C G C T G G C G G C G T G C	49029	16S	

C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	.	.	C	.	C	T	T	C	G	G	.	G	G	.	A	G	C		Consensus #1	
C	E	A	A	T	A	C	A	T	G	C	A	A	A	G	T	C	G	A	G	C	G	-	-	C	C	C	T	T	C	G	G	-	G	G	C	C	A	G	C	Majority

	50	60	70	80																																						
41	C	T	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	G	T	C	T	C	G	G	A	G	G	C	C	A	G	C	43030						
21	C	T	A	A	T	A	C	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	A	G	-	C	C	C	T	T	C	G	G	-	G	G	C	T	A	G	C	49025
41	C	T	A	A	T	A	C	C	A	T	G	C	A	A	G	T	C	G	A	G	C	G	A	-	C	C	C	T	T	C	G	G	-	G	G	T	C	A	G	C	49029	

G	G	C	G	G	A	C	G	G	T	G	A	G	.	A	A	C	A	C	G	T	G	G	G	.	A	A	T	C	.	G	C	C	.	.	C	.	G		Consensus #1
C	C	C	C	C	A	C	C	C	C	T	C	A	C	T	A	A	C	A	C	G	T	G	G	T	A	A	T	C	T	G	C	C	T	T	C	A	G		Majority

	90	100	110	120		
81	G	G	G	G	G	43030
	G	G	G	G	G	16S
59	G	G	G	G	G	49025
	G	G	G	G	G	16S
79	G	G	G	G	G	49029
	G	G	G	G	G	16S

C	G	G	A	T	A	A	C	.	C	.	G	G	A	A	C	G	G	G	.	G	C	T	A	A	.	G	C	C	G	G	A	T	A	.	C	Consensus #1
C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	A	A	T	G	C	C	G	G	A	T	A	X	Majority	

	130	140	150	160	
121	G C C G G A A T A A C C G C C C G G A A A C G G G C G C T A A A A G C C C G G A T A C	43030	16S		
99	A C C T G G A A T A A C C A C C T C C G G A A A C G G G T G C C T A A T G C C G G A T A -	49025	16S		
119	A C C G G A A T A A C G C C C T G G A A A C G G G T G C C T A A T G C C G G A T A G	49029	16S		

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

. C G . G . A G G C A T C T . C T . G G . A A G C A A . T Consensus #1
 G C A C G C G A G X A G G C A T C T X C T T G C G G G G A A A A G G T G C A A X T Majority

	170	180	190	200	
161	G C C C G C G A G	G A G G C A T C T	T C T T G C C G G G G	G A A G G C C C A A T	T 43030 16s
138	A T A C A C G G T	A G G C A T C T	A C T T G T G T G	A A A G A T G C C A A C	T 49025 16s
159	G C A - G C G A G	C A G G C A T C T	G C T C G C T G G G	A A A G G T G C C A A G	T 49029 16s

G . . . C G C . G A . . . G A G G A G C C C G C G G C G C A T T A G C T . G T T G Consensus #1
 G C A T C G C T G A G A G A G G A G C C C G C G G C G C A T T A G C T A G T T G Majority

	210	220	230	240	
201	G G G T C G C T G A G A G A G G A G C C C C G C G G C G C A T T A G C T A G T T G	43030 16s			
178	G C A T C G C T G A G A G A G G A G C C C C G C G G C G C A T T A G C T A G T T G	49025 16s			
198	G C A C C G C A G A T G G A G G A G C C C G C G G C G C A T T A G C T G T T G	49029 16s			

G . G . G G T A A C G G C . C A C C A A G G C G A C G A T G C G T A G C C G A C Consensus #1
 G T G G G G T A A C G G C T C A C C A A G G C G A C G A T G C G T A G C C G A C Majority

	250	260	270	280	
241	G C G G G T A A C G G C C	C A C C A A G G C G A C G A T G C G T A G C C G A C	43030 16s		
218	G T G A A C G G C T C A C C A A G G C G A C G A T G C G T A G C C G A C	49025 16s			
238	G T G G G T A A C G G C T C A C C A A G G C G A C G A T G C G T A G C C G A C	49029 16s			

C T G A G A G G G T G . . C G G C C A C A C T G G G A C T G A G A C A C G G C C Consensus #1
 C T G A G A G G G T G A C C C G G C C A C A C T G G G A C T G A G A C A C G G C C Majority

	290	300	310	320	
281	C T G A G A G G G T G A C C G G C C A C A C T G G G A C T G A G A C A C G G C C	43030 16s			
258	C T G A G A G G G T G A C C G G C C A C A C T G G G A C T G A G A C A C G G C C	49025 16s			
278	C T G A G A G G G T G G A C G G C C A C A C T G G G A C T G A G A C A C G G C C	49029 16s			

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A Consensus #1
 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A Majority

330 340 350 360

321 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A 43030 16s
 298 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A 49025 16s
 318 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A 49029 16s

T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A Consensus #1
 T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A Majority

370 380 390 400

361 T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A 43030 16s
 338 T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A 49025 16s
 358 T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A 49029 16s

A G G C C T T C G G G T T G T A A A G C T C . G T . . C T C G G G . A G A G C G Consensus #1
 A G G C C T T C G G G T T G T A A A G C T C T G T T G C T C G G G G A G A G C G Majority

410 420 430 440

401 A G G C C T T C G G G T T G T A A A G C C T C T G T T G C T C G G G G A G A G C G 43030 16s
 378 A G G C C T T C G G G T T G T A A A G C C T C T G T T G C T C G G G G A G A G C G 49025 16s
 398 A G G C C T T C G G G T T G T A A A G C C T C A G T C A C T C G G G A A G A G C G 49029 16s

. C A . G G . G . . T G G A A A G C . C C . T G . G A G A C G G T A C C G A G . Consensus #1
 G C A A G G G A G T G G A A A A G C C C C T T G X G A G A C G G T A C C G A G T Majority

450 460 470 480

441 G C A T G G G G A T G G A A A G C C C C G T G C G A G A C G G T A C C G A G T 43030 16s
 418 A C A A G G A G A G T G G A A A G C C T T G T G A G A C G G T A C C G A G T 49025 16s
 438 G C A A G G G A G T G G A A A G C C C C T T G A G A G A C G G T A C C G A G A 49029 16s

Alignment Report of Untitled ClustalV (Weighted)

Alignment 1

Friday, September 05, 2003 9:42 AM

G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A Consensus #1
 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A Majority

481 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A 520 43030 16s
 458 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A 49025 16s
 478 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A 49029 16s

. A C G T A G G G G C . A G C G T T G T C C G G A A T C A C T G G G . C G T A Consensus #1
 T A C G T A G G G G C A A G C G T T G T C C G G A A T C A C T G G G - C G T A Majority

521 A A C G T A G G G G C G A G C C G T T G T C C G G A A T C A C T G G G - C G T A 560 43030 16s
 498 T A C G T A G G G G C A A G C C G T T G T C C G G A A T C A C T G G G G C G T A 49025 16s
 518 T A C G T A G G G G C A A G C C G T T G T C C G G A A T C A C T G G G - C G T A 49029 16s

A A G . G T G C G T A . G C G G T . G . G . . . G T C . G . . . T G A A A G T C Consensus #1
 A A G C G T G C G T A G G C G G T T G X G T A A G T C T G G A A G T G A A A G T C Majority

560 A A G G T G C G T A G G C G G T C G A G C A A G T C T G G A G T G A A A G T C 600 43030 16s
 538 A A G C G T G C G T A N G C G G T T G T G T A A G T C T G A A C T G A A A G T C 49025 16s
 557 A A G C G T G C G T A G G C G G T T G C G T G T C C G G G T G A A A A G T C 49029 16s

C A . G G C T C . A C C . T G G G . . . G C . T T G G A A A C T G C . T . . A C Consensus #1
 C A X G G C T C A A C C X T G G G A A T G C T T T G G A A A C T G C X T G - A C Majority

600 C A T G G C T C A A C C A T G G G A T G G C T T T G G A A A C T G C T T G - A C 640 43030 16s
 578 C A A G G C T C N A C C T T G G G N A T G C T T T G G A A A C T G C A T G G A C 49025 16s
 597 C A G G G C T C A A C C C T G G G A A T G C C T T G G A A A C T G C G T A - A C 49029 16s

Alignment 1

September 20, 1966

T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	.	A	G	G	.	.	A	A	T	T	C	C	.	C	G	T	G	T	.	A	.	C	G	C	Consensus	#1
T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	A	G	G	G	G	A	A	T	T	C	C	X	C	C	G	T	G	T	-	A	G	C	G	Majority	

	650	660	670	680
639	T T G A G T G C T G G A G A G G C A A G G G G A A T T C C A C G T G T - A G C G	43030	16S	
618	T T G A G T G C T G G A G A G G C N A G G C N A A T T C C N C G T G T T A C C G	49025	16S	
636	T T G A G T G C T G G A G A G G C A A G G G G A A T T C C G C G T G T - A G C G	49029	16S	

GTG . AA . TGGC . . A . A . ATG . GGAGGAATA C C A G T G G C . A Consensus #1
CTCYAA - TGGCGT - AGAATA TGTGGAGGAATA C C A G T G G C G A Majority

	690	700	710	720	
678	G T G A A - T G C G T - A G A	A T G T G G A G G A A T A C C A G T G G C G A	43030	16S	
658	G T G N A A A T G C G N T A N A T A T G T G G A G T G G C N A	49025	16S		
675	G T G G A A - T G C G T - A G A T A T G C G G A G G A A T A C C A G T G G C G A	49029	16S		

A . G C G C C T T . G C T G G A C A G T G . A C T G A C G C T G A . G G C A C G Consensus #1
A Y C C C C C T T - G C T G G A C A G T G - A C T G A C G C T G A - G G C A C G Majority

	730	740	750	760
716	A R G C G C C T T - G C T G G A C A G T G - A C T G A C G C T G A - G G C A C G	43030	168	
698	A N G C G C C T T T G C C T G G A C A G T G G A C T G A C C G C T G A A G G C A C G	49025	168	
713	A G G C G C C T T - G C C T G G A C A G T G - A C T G A C C G C T G A - G G C A C G	49029	168	

[illegible]

	770	780	790	800	
753	A A - G C G T G G G G A G C A A	- - - - -	- - - - -	- - - - -	43030 16S
738	A A A A N C G T G G G A N C A A	C N G G A T T A N A T C C C C N A N G C G N	- - - - -	- - - - -	49025 16S
750	A A A - G C G T G G G G A G C A A	- - - - -	- - - - -	- - - - -	49029 16S

Alignment 1

Alignment Report of Unfiled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

Consensus #1
Majority

810 820 830 840

769 - - - - - A C A G G A T T A G A T . C C C . . . G T A G T C C . . C 43030 16s
 778 G G G A A G C A A A C A G G A T T A G A T T C C C N T T G T A G T C C C G C C 49025 16s
 766 - - - - - A C A G G A T T A G A T A C C C T G - G T A G T C C - A C G 49029 16s

Consensus #1
Majority

850 860 870 880

797 C C G T A A . C . A T G A G T . C T . A G . T G T T G G G G G C A C C C 43030 16s
 818 C C G T A A C G A T G A G T G C T - A G G T G T T G G G G G G A C A C A C C C 49025 16s
 794 C C G T A A A C G A T G A G T G C T - A G G T G T T G G G G G G T A C C A C C C 49029 16s

Consensus #1
Majority

890 900 910 920

836 - C A G T G C C G A A G G A A A M C C A A T A A G C A C T C C G C C T G G G A 43030 16s
 858 - C A N T G C G N G G A A A C C C A A T A A G C A C T C C G C C T G G G A 49025 16s
 833 T C A G T G C C G A A G G A A A C C C A A T A A G C A C T C C G C C T G G G A 49029 16s

Consensus #1
Majority

930 940 950 960

875 G T A C G G T C G C A A G A C T G A A A C T C A A A G G A A T T G A C G G G G G 43030 16s
 896 G T G G G T C N C A A G A C T G A A N C T C A A A G G A A T T G A C G G G G G 49025 16s
 873 G T A C G G T C G C A A G A C T G A A A C T C A A A G G A A T T G A C G G G G G 49029 16s

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

Alignment 1

C C C G C A C A A G C A G T G G A G C A T . T G G T T T A A . T C G A A G C A A Consensus #1
C C C G C A C A A G C A G T G G A G C A T T T A A T T C G A A G C A A Majority

	970	980	990	1000	
915	C C C G C A C A A G C A G T G G A G C A T G T G G T T T A A A T C G A A G C A A				43030 16s
936	C C C G C A C A A G C A G T G G A G C A T N T G G T T T A A T T C G A A G C A A				49025 16s
913	C C C G C A C A A G C A G T G G A G C A T G T G G T T T A A T T C G A A G C A A				49029 16s

C G C G A A G A A C C T T A . C A G G G C T . G A C A T C C C . C T G A C . . Consensus #1
C G C G A A G A A C C T T A C C A G G G C T X G A C A T C C C T C T G A C A G C Majority

	1010	1020	1030	1040	
955	C G C G A A G A A C C T T A C C A G G G C T T G A C A T C C C T C T G A C A C C				43030 16s
976	C G C G A A G A A C C T T A C C A G G G C T T N G A C A T C C C T C T G A C C G G				49025 16s
953	C G C G A A G A A C C T T A N C A G G G C T C G A C A T C C C C C T G A C A G C				49029 16s

. . C A G A G A T G T C C C C T T C G G G G C A G . G G A G A C A G G T Consensus #1
C G C A G A G A T G X G G X T T C C C C T T C G G G G C A G A G G A C A G G T Majority

	1050	1060	1070	1080	
995	C T C A G A G A T G A G G G T C C C C T T C G G G G C A G A G G A C A G G T				43030 16s
1016	T G C A G A G A T G T A C C T T C C C C T T C G G G G C A G A G G A C A G G T				49025 16s
993	C G C A G A G A T G C G G T T T C C C C T T C G G G G C A G G G A G A C A G G T				49029 16s

G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G Consensus #1
G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G Majority

	1090	1100	1110	1120	
1035	G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G				43030 16s
1056	G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G				49025 16s
1033	G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G				49029 16s

Alignment Report of Untitled ClustalV (Weighted)

Alignment 1

Friday, September 05, 2003 9:42 AM

T T . A G T C C C G C A A C G A G C G C C A C C C C T T G A . C T G T G T T A C C Consensus #1
 T T A A G T C C C G C A A C G A G C G C C A A C C C T T G A X C T G T G T T A C C Majority

	1130	1140	1150	1160	
1075	T T C A G T C C C G C A A C G A G C G C C A A C C C T T G A C C T G T G T T A C C				43030 16s
1096	T T A A G T C C C G C A A C G A G C G C C A A C C C T T G A T C T G T G T T A C C				49025 16s
1073	T T A A G T C C C G C A A C G A G C G C C A A C C C T T G A A C T G T G T T A C C				49029 16s

A G C . C G T . . . G G . G G G G A C T C A C A G . T G A C T G C C G G C C G T A Consensus #1
 A G C A C G T T G A G G T G G G G A C T C A C A G G T G A C T G C C G G C C G T A Majority

	1170	1180	1190	1200	
1115	A G C G C G T T G A G G C G G G G A C T C A C A G G T G A C T G C C G G C C G T A				43030 16s
1136	A G C A C G T T G T G G T G G G G A C T C A C A G G T G A C T G C C G G C C G T A				49025 16s
1113	A G C A C G T G A A G G T G G G G A C T C A C A G T T G A C T G C C G G C C G T A				49029 16s

A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C Consensus #1
 A G T C G G A G G A A G G C G G G A T G A C G T C A A A T C A T C A T G C C C Majority

	1210	1220	1230	1240	
1155	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C				43030 16s
1176	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C				49025 16s
1153	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C				49029 16s

. T . A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G . A C Consensus #1
 T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G T A C Majority

	1250	1260	1270	1280	
1195	C T G A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G A A C				43030 16s
1216	T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G T A C				49025 16s
1193	T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G T A C				49029 16s

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

A A . G G G A . G C G A . . C C G C G A G G . G G A G C . A A . C C . . . A A A Consensus #1
A A C G G G A A G C G A A G C C G C G A G G T G G A G C C A A A A C C C A A A A Majority

1290 1300 1310 1320
1235 A A A G G G A G C C G A A G C C G C G A G G C G G A G C G A A A C C C A A A A 43030 16s
1256 A A C G G G A A G C C G A A G C C G C G A G G T G G A G C C A A A A A A 49025 16s
1233 A A C G G G A A G C G A G A C C G C G A G G T G G A G C C A A A C C C T G A A A A 49029 16s

G C C G . T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A Consensus #1
G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A Majority

1330 1340 1350 1360
1275 G C C G C T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 43030 16s
1296 G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 49025 16s
1273 G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 49029 16s

T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C Consensus #1
T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C Majority

1370 1380 1390 1400
1315 T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 43030 16s
1336 T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 49025 16s
1313 T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 49029 16s

G G T G A A T . C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C Consensus #1
G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C Majority

1410 1420 1430 1440
1355 G G T G A A T A C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 43030 16s
1376 G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 49025 16s
1353 G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 49029 16s

Alignment 1

Alignment Report of Untitled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G . G G T A A C C Consensus #1
A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C Majority

1450 1470 1480
↓
1395 A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C 43030 16s
1416 A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C 49025 16s
1393 A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C 49029 16s

. T G G A G C C A G C C G C C G A A G G T G G G G T . G A T G A T T G Consensus #1
C X T X T X G G G A G C C A G C C C G C C G A A G G T G G G G T T G A T G A T T G Majority

1490 1500 1510 1520
1435 C C T G T G G G A G C C C A G C C C G C C G A A G G T G G G G T C G A T G A T T G 43030 16s
1456 G T T A T - - G G A G C C C A G C C C G A A G G T G G G G T T G A T G A T T G 49025 16s
1433 C G T - C A G G G A G C C C A G C C C G C C G A A G G T G G G G T T G A T G A T T G 49029 16s

G G G T G A A G T C G T A A C A A G G T A G C C G T Consensus #1
G G G T G A A G T C G T A A C A A G G T A G C C G T Majority

1530 1540
1475 G G G T G A A G T C G T A A C A A G G T A G C C G T 43030 16s
1494 G G G T G A A G T C G T A A C A A G G T A G C C G T 49025 16s
1472 G G G T G A A G T C G T A A C A A G G T A G C C G T 49029 16s

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 2

Sequence, 49029 16S
5 AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCCTAATACATGCAAGTCGAGCGGACCCCTTCGGGGTCAGCGG
CGGACGGGTGAGTAACACGTGGGTAAATCTGCCCAAATGACCGGAATAACGCCTGGAAACGGGTGCTAATGCCGATAGGC
AGCGAGCAGGCATCTGCTCGCTGGGAAAGGTGCAACCGCAGATGGAGGAGCCCGCGGCATTAGCTGTTGGTG
GGGTAAACGGCTCACCAAGGCACGATGCGTAGCCGACCTGAGAGGTTGGACGGCCACACTGGGACTGAGACACCGCCCCAG
ACTCCTACGGGAGGCAGTAGGGAATCTTCGGCAATGGGCGCAAGCCTGACCGAGCAACGCCGCGTGAGCGGAAGAAG
CCTTCGGGTTGTAAAGCTCAGTCACTCGGGAAGAGCGGCAAGGGAGTGGAAAGCCCTTGAGAGACGGTACCGAGAGAG
10 GAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGC
GTGCGTAGGCGGTTGCCGTGTCTCCGGGTGAAAGTCCAGGGCTCAACCCCTGGGAATGCCCTTGAAACTGCGTAACCTTGAG
TGCTGGAGAGGCAAGGGGAATTCCGCGTGTAGCGGTGGAATGCGTAGATATGCGGAGGAATACCAAGTGGCGAAGGCGCCT
TGCTGGACAGTGACTGACGCTGAGGCACGAAGCGTGGGAGCAACACAGGATTAGATAACCCCTGCTAGTCCACGCGCGTAA
CGATGAGTGTAGGTGTTGGGGGTACCAACCTCAGTGCCGAAGGAAACCCCAATAAGCACTCCGCCCTGGGGAGTACGGTC
15 GCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCCGCAACAAGCAGTGGAGCATGTGGTTTAAATTCGAAGCAACGCGAAGA
ACCTTANCAGGGCTCGACATCCCCCTGACAGCCGACAGATGCGGTTTCCCTTCGGGGCAGGGAGACAGGTGGTGCAATG
GTTGTCGTCAAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGAACTGTGTACCAAGCACGTCG
AAGGTGGGACTCACAGTTGACTGCCGGCGTAAGTCGGAGGAAGCGGGGATGACGTCAAATCATCATGCCCTTTATGTC
CTGGGCTACACAGTGCTACAATGGGCGGTACAACGGGAAGCGAGACCCGCGAGGTGGAGCAAAACCCCTGAAAGCCGTTCCG
20 TAGTTCGGATTGCAGGCTGCAACTCGCCCTGCATGAAGCCGGAAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATC
CGTTCCTCCGGGCTTGTAACACACCCCGCTCACACACGAGAGTCGGCAACACCCGAAAGTCGGTGGGGTAACCCCGTCAGGG
AGCCAGCCCCGAAAGGTGGGTTGATGATTGGGGTGAAGTCGTAAACAAGGTAGCCGT

Figure 3

49025 16S
5 GACGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAGCCCTTCGGGGCTAGCGGGGACGGGTGAGTAACACGT 80
GGGCAATCCGCTTTCAGACTGGAAATAACACTCGGAAACGGGTGCTAATGCCGGATAATACACGGGTAGGCATCTACTTG 160
TGTGAAAGATGCAACTGCATCGCTGAGAGAGAGCCCGCGGCATTAGCTAGTTGGTGAGGTAAACGGCTCACCAAGGC 240
GACGATGCGTAGCCGACCTGAGAGGGTGACCCGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAG 320
TAGGGAATCTTCCGCAATGGGCGCAAGCCCTGACGGAGCAACGCCCGGTGAGCGAAGAAAGCCCTTCGGGTTGTAAAGCTCT 400
GTTGCTCGGGGAGAGCGACAAAGGAGAGTGGAAGCTCCTTGTGAGACGGTACCGAGTGAGGAAGCCCCGGCTAACTACGT 480
GCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGCGTGCGTANGCGGTTGTGTA 560
AGTCTGAACTGAAAGTCCAAAGGCTCNACCTTGGGNATGCTTGGAAACTGCTGACTTGAGTGTCTGGAGAGGCNAGGCN 640
AATTCCNCGTGTACCGGTGNAAATGCCGNTANATATGTGGAGGAATACCAAGTGGCNAANGCGCCTTTGCTGGACAGTGGA 720
CTGACGCTGAAGGCACGAAANCGTGGGANCAACNGGATTANATCCCNAAANGCGGGGAAGCAACACAGGATTAGATT 800
CCCNTTGTAGTCCCGCCCGTAANCNATGAGTACTTAGTTGTTGGGGAACACACCCCAANTGCGNGGAAACCCCAATAAG 880
CACTCCGCTGGGAGTGGGTCNCAAGACTGAANCTCAAAGGAATTGACGGGGGCGCCGCAAGCAGTGGAGCATNTGG 960
TTTAAATTCGAAGCAACGGAAGAACCTTACCAGGGCTNGACATCCCTCTGACCGGTGCAGAGATGTACCTTCCCTTCGGG 1040
GCAGAGGAGACAGGTGGTGCAATGGTTGTCTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC 1120
TTGATCTGTGTTACCAGCACGTTGTGGTGAGTGTGGGACTCACAGGTGACTGCCGGCGTAAGTCGGAGGAAGCGCGGATGACGT 1200
CAAAATCATATGCCCTTTATGTCCTGGGCTACACACGTGCTACAATGGGCGGTACAACGGGAAGCGAGCCCGAGGTGG 1280
AGCAAAACCTAAAAGCCGTTTCGTAGTTTCGGATTGCAAGGTGCAACTCGCCTGCTAAGAGCCCGGAAATTGCTAGTAATCGC 1360
GGATCAGCATGCCGCGGTGAATCCGTTCCCGGGCCTTGTAACACCGGCCGTCAACCAAGAGTCGGCAACACCCCGAA 1440
GTCGGTGAGGTAAACCGTTATGGAGCCAGCCCGCAAGGTGGGTTGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGT 1519

Figure 4

43030 16S
AGAGTTTGATCCTGGCTCAGGACGAACGGTGGCGGGTGCCTAATACATGCAAGTCGAGCGGGTCTCTTTCGGAGGCCAGC
5 GCGGACGGGTGAGGAACACGTGGGTAATCTGCCCTTTCAGGCCGGAAATAACGCCCGGAAACGCGCGCTAAAGCCGGATAC
GCCCCGAGGAGGCATCTTCTTTCGGGGAAGGCCCAATTGGGTCGCTGAGAGAGGAGCCCCGCGGCATTAGCTAGTTG
GCGGGTAACGGCCCCACCAAGGCACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCC
CAGACTCCTACGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGCAAGCCTGACCGAGCAACGCCCGCTGAGCGGAAGA
AGGCCCTTCGGGTTGTAAAGCTCTGTTGCTCGGGGAGAGCGGCATGGGGATGGAAGCCCCGTGCGAGACGGTACCGAGT
10 GAGGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAAACGTAGGGGCGAGCGTGTGTCCGGAATCAC'TGGGCGTAA
AGGTGCGTAGGCCGTGAGCAAGTCTGGAGTGAAAGTCCATGGCTCAACCATGGGATGGCTTTGGAAACTGCTTGACTT
GAGTGTGGAGAGCAAGGGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCAAGTGGCGAARGCG
CCTTGTGACAGTGACTGACGCTGAGGCACGAAGCGTGGGAGCAAAACAGGATTAGATACCTGCTGCTGACCGCGT
15 AAACGATGAGTGCTAGGTGTTGGGGGACACACCCAGTGCAGGAAAGCAATAGCACTCCGCTGGGAGTACGG
TCGCAAGACTGAACCTCAAAGGAATTGACGGGGGCCCCGACAAAGCAGTGGAGCATGTGGTTTAAATCGAAGCAACCGCAA
GAACCTTACCAGGGCTTGACATCCCTCTGACACCCCTCAGAGATGAGGGTCCCTTCGGGGCAGAGGACAGGTGGTGCA
TGGTGTGTCGTGCTCGTGAGATGTTGGGTTCAGTCCCGCAACGAGCGCAACCCCTTGACCTGTGTACCAGCGCG
TTGAGGCGGGACTCACAGGTGACTGCCGGCGTAAGTCGGAGGAAGCGGGGATGACGTCAAATCATCATGCCCTGATG
TCCTGGGCTACACACGTGCTACAA'TGGGCGGAACAAAGGAGGCGAAGCCCGAGGCGGAGCGAAACCCAAAAGCCGCT
CGTAGTTCGGATTGCAGGCTGCAACTCGCCTGCAATGAAGCCGGAATTGCTAGTAATCGCGGATCAGCATGCCCGCGGTGAA
20 TACGTTCCCCGGCCTTGTAACACACCGCCCGTCACACCAGAGTTCGGCAACACCCGAAGTCGGTGAGGTAAACCCCTGTG
GGGAGCCAGCCCGCAAGGTGGGTCGATGATTGGGTGAAGTCGTAAACAAGGTAGCCGT

Figure 5: Shc polynucleotide sequence alignments

Cloned ac 43030: Cloned *Alicyclobacillus acidocaldarius* ATCC43030
 Cloned at 43030: Cloned *Alicyclobacillus acidoterrestris* ATCC49025
 Blast ac: sequence of *A. acidocaldarius* got from the blast database
 Blast at: sequence of *A. acidocaldarius* got from the blast database

Primer and probe ranges were highlighted red

```

10      G G G G G T T G G A T G T T C C A G G C Majority
      -----+-----
              10                      20
      -----+-----

15      1 G G G G G T T G G A T G T T A C A G G C cloned ac 43030 shc
      1 G G A G G A T G G A T G T T T C A G G C Blast ac shc
      1 G G A G G G T G G A T G T T C C A G G C cloned at 49025 shc
      1 G G G G G T T G G A T G T T C C A G G C Blast at shc

20      T T G T A T T T C T C C A G T G T G G G Majority
      -----+-----
              30                      40
      -----+-----

25      21 T T C C A T C T C G C C C G T G T G G G cloned ac 43030 shc
      21 T T C C A T C T C G C C G G T G T G G G Blast ac shc
      21 G A G T A T T T C T C C A A T C T G G G cloned at 49025 shc
      21 G A G T A T T T C T C C A A T C T G G G Blast at shc

30      A T A C T G G C T T G G C C G T G T T G Majority
      -----+-----
              50                      60
      -----+-----

35      41 A C A C G G G T C T C G C C G T G C T C cloned ac 43030 shc
      41 A C A C G G G C C T C G C C G T G C T C Blast ac shc
      41 A T A C T G G C T T G A C C G T C T T G cloned at 49025 shc
      41 A T A C T G G C T T G A C C G T C T T G Blast at shc

40      G C G C T G C G T T C T G C T G G G T T Majority
      -----+-----
              70                      80
      -----+-----

45      61 G C G C T G C G C G C T G C G G G G C T cloned ac 43030 shc
      61 G C G C T G C G C G C T G C G G G G C T Blast ac shc
      61 G C A C T G C G T T C G G C T G G A T T cloned at 49025 shc
      61 G C A C T G C G T T C G G C T G G A T T Blast at shc

50      T C C G G C C G A T C A T - G C C G G G Majority
      -----+-----
              90                      100
      -----+-----

55      81 T C C G G C C G A T C A C T G A C C G G cloned ac 43030 shc
      81 T C C G G C C G A T C A C - G A C C G C Blast ac shc
      81 G C C A C C A G A T C A T - C C A G C G cloned at 49025 shc
      81 G C C A C C A G A T C A T - C C A G C G Blast at shc
  
```

Figure 5: Shc polynucleotide sequence alignments (continued)

		T T G G T T A A G G C - - G G G T G A G Majority														
5		-----+-----+-														
		110							120							
		-----+-----+-														
	101	T T G G T C A A G G C T G G G C T G A A cloned ac 43030 shc														
	100	T T G G T C A A G G C - - G G G C G A G Blast ac shc														
10	100	C T G A T T A A A G C - - G G G T G A G cloned at 49025 shc														
	100	C T G A T T A A A G C - - G G G T G A G Blast at shc														
		T G G T T G T T G G G T C G G C A G A T Majority														
		-----+-----+-														
15		130							140							
		-----+-----+-														
	121	T G G C T G T T G G A C C G G C A G A T cloned ac 43030 shc														
	118	T G G C T G T T G G A C C G G C A G A T Blast ac shc														
	118	T G G T T G G T C A G T A A A C A A A T cloned at 49025 shc														
20	118	T G G T T G G T C A G T A A A C A A A T Blast at shc														
		T C T C G T G G C T G G C G A C T G G G Majority														
		-----+-----+-														
		150							160							
		-----+-----+-														
25	141	C A C C G T G C C G G G C G A T T G G G cloned ac 43030 shc														
	138	C A C G G T T C C G G G C G A C T G G G Blast ac shc														
	138	T C T C A A G G A T G G C G A C T G G A cloned at 49025 shc														
	138	T C T C A A G G A T G G C G A C T G G A Blast at shc														
30		A G G T T C G T C G C C G G A A G G T G Majority														
		-----+-----+-														
		170							180							
		-----+-----+-														
35	161	T G G T G A A G C G C C C G A A C C T C cloned ac 43030 shc														
	158	C G G T G A A G C G C C C G A A C C T C Blast ac shc														
	158	A A G T T C G T C G A C G C A A G G C G cloned at 49025 shc														
	158	A A G T T C G T C G A C G C A A G G C G Blast at shc														
40		A A A C C G G G C G G T T T G G C G T T Majority														
		-----+-----+-														
		190							200							
		-----+-----+-														
45	181	A A C C C G G G C G G C T T C G C G C T cloned ac 43030 shc														
	178	A A G C C G G G C G G G T T C G C G T T Blast ac shc														
	178	A A A C C A G G C G G T T G G G C A T T cloned at 49025 shc														
	178	A A A C C A G G C G G T T G G G C A T T Blast at shc														
		T G A G T T C G A C T G C G T G T A C T Majority														
		-----+-----+-														
50		210							220							
		-----+-----+-														
	201	C C A G T T C G A C A A A C G T G T A C T cloned ac 43030 shc														
	198	C C A G T T C G A C A A A C G T G T A C T Blast ac shc														
55	198	T G A A T T C C A C T G C G A A A A C T cloned at 49025 shc														
	198	T G A A T T C C A C T G C G A A A A C T Blast at shc														

Figure 5: Shc polynucleotide sequence alignments (continued)

		A C C C G G A C G T G G A C G A T A C G	Majority
		-----+-----+-----	
5		230	240
		-----+-----+-----	
	221	A T C C G G A C G T G G A C G A C A C G	cloned ac 43030 shc
	218	A C C C G G A C G T G G A C G A C A C G	Blast ac shc
	218	A C C C A G A C G T C G A C G A T A C G	cloned at 49025 shc
10	218	A C C C A G A C G T C G A C G A T A C G	Blast at shc
		G C G G T G G T C G T C T T G G C G C T	Majority
		-----+-----+-----	
		250	260
		-----+-----+-----	
	241	G C C G T C G T C A T C T G G G C G C T	cloned ac 43030 shc
	238	G C C G T C G T G G T G T G G G C G C T	Blast ac shc
	238	G C G A T G G T C G T C T T G G C G C T	cloned at 49025 shc
	238	G C G A T G G T C G T C T T G G C G C T	Blast at shc
20		C A A T G G C C T T C G A T T G C C G G	Majority
		-----+-----+-----	
		270	280
		-----+-----+-----	
25	261	C A A C A C G C T G C G A C T C C C G G	cloned ac 43030 shc
	258	C A A C A C C C T G C G C T T G C C G G	Blast ac shc
	258	C A A T G G C A T T C A A T T G C C G G	cloned at 49025 shc
	258	C A A T G G C A T T C A A T T G C C G G	Blast at shc
30		A T G A G G G G C G G C G T C G T G A C	Majority
		-----+-----+-----	
		290	300
		-----+-----+-----	
	281	A C G A G C G C C G C A G G C G A G A C	cloned ac 43030 shc
	278	A C G A G C G C C G C A G G C G G G A C	Blast ac shc
	278	A T G A A G G G A A G C G T C G T G A C	cloned at 49025 shc
	278	A T G A A G G G A A G C G T C G T G A C	Blast at shc
40		G C C T T G A C G C G T G G C T T C C G	Majority
		-----+-----+-----	
		310	320
		-----+-----+-----	
	301	G C C A T G A C G A A G G G A T T C C G	cloned ac 43030 shc
	298	G C C A T G A C G A A G G G A T T C C G	Blast ac shc
45	298	G C A T T G A C C C G T G G C T T C C G	cloned at 49025 shc
	298	G C A T T G A C C C G T G G C T T C C G	Blast at shc
		T T G G T T T G T C G G G A T G C A G A	Majority
		-----+-----+-----	
50		330	340
		-----+-----+-----	
	321	C T G G A T T G T C G G C A T G C A G A	cloned ac 43030 shc
	318	C T G G A T T G T C G G C A T G C A G A	Blast ac shc
	318	T T G G T T G C G C G A G A T G C A G A	cloned at 49025 shc
55	318	T T G G T T G C G C G A G A T G C A G A	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		G T T C G A A C G G G G G C T G G G G C	Majority
		-----+-----+-----	
5		350 360	
		-----+-----+-----	
	341	G C T C G A A C G G C G G C T G G G G C	cloned ac 43030 shc
	338	G C T C G A A C G G C G G T T G G G G C	Blast ac shc
	338	G T T C G A A C G G G G G C T G G G G C	cloned at 49025 shc
10	338	G T T C G A A C G G G G G C T G G G G C	Blast at shc
		G C A T A C G A T G T G G A C A A C A C	Majority
		-----+-----+-----	
		370 380	
		-----+-----+-----	
15	361	G C A T A C G A C G T C G A C A A C A C	cloned ac 43030 shc
	358	G C C T A C G A C G T C G A C A A C A C	Blast ac shc
	358	G C A T A C G A T G T G G A C A A C A C	cloned at 49025 shc
	358	G C A T A C G A T G T G G A C A A C A C	Blast at shc
20		G C G T G A T T T G C C G A A - T C G G	Majority
		-----+-----+-----	
		390 400	
		-----+-----+-----	
25	381	G A G C G A T C T C C C G A A - C C A C	cloned ac 43030 shc
	378	G A G C G A T C T C C C G A A - C C A C	Blast ac shc
	378	G C G T C A G T T G A C C A A - T C G G	cloned at 49025 shc
	378	G C G T C A G T T G A C C A A A T C G G	Blast at shc
30		A T T C C G T T T T - G C G A C T T C G	Majority
		-----+-----+-----	
		410 420	
		-----+-----+-----	
35	400	A T C C C G T T C T - G C G A C T T C G	cloned ac 43030 shc
	397	A T C C C G T T C T - G C G A C T T C G	Blast ac shc
	397	A T T C C A T T T T - G C A A C T T C G	cloned at 49025 shc
	398	A T T C C A T T T T T G C G A C T T C G	Blast at shc
40		G - C G A A G T G A T T G A T C C G C C	Majority
		-----+-----+-----	
		430 440	
		-----+-----+-----	
45	419	G - C G A A G T G A C C G A T C C G C C	cloned ac 43030 shc
	416	G - C G A A G T G A C C G A T C C G C C	Blast ac shc
	416	G - C G A A G T G A T T G A T C C G C C	cloned at 49025 shc
	418	G G C G A A G T G A T T G A T C C G C C	Blast at shc
50		G T C G G A A G A C G T C A C C G C C C	Majority
		-----+-----+-----	
		450 460	
		-----+-----+-----	
	438	G T C G G A A G A C G T C A C C G C C C	cloned ac 43030 shc
	435	G T C A G A G G A C G T C A C C G C C C	Blast ac shc
	435	A T C G G A A G A C G T C A C C G C C A C	cloned at 49025 shc
55	438	A T C G G A A G A C G T C A C C G C C A C	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		A C G T G T T T G G A G T G T T T C G G C	Majority
		-----+-----+-----	
5		470 480	
		-----+-----+-----	
	458	A C G T G C T C <u>G A G T G T T T C G G C</u>	cloned ac 43030 shc
	455	A C G T G C T C <u>G A G T G T T T C G G C</u>	Blast ac shc
	455	A C G T C T T G <u>G A G T G C T T C G G C</u>	cloned at 49025 shc
10	458	A C G T C T T G <u>G A G T G C T T C G G C</u>	Blast at shc
		A G C T T T G G G T A C G A C G A G G C	Majority
		-----+-----+-----	
		490 500	
		-----+-----+-----	
15	478	<u>A G C T T</u> C G G G T A C G A C G A C G C	cloned ac 43030 shc
	475	<u>A G C T T</u> C G G G T A C G A T G A C G C	Blast ac shc
	475	<u>A G C T T</u> T G G G T A C G A C G A G G C	cloned at 49025 shc
	478	<u>A G C T T</u> T G G G T A C G A C G A G G C	Blast at shc
20		C T G G A A G G T G A T T C G G C G G G	Majority
		-----+-----+-----	
		510 520	
		-----+-----+-----	
25	498	C T G G A A G G T G A T C C A G C G C G	cloned ac 43030 shc
	495	C T G G A A G G T C A T C C G G C G C G	Blast ac shc
	495	A T G G A A G G T G A T T C G C A A G G	cloned at 49025 shc
	498	A T G G A A G G T G A T T C G C A A G G	Blast at shc
30		C G G T G G A G T A T C T C A A G G G G	Majority
		-----+-----+-----	
		530 540	
		-----+-----+-----	
35	518	C G G T G G C G T A C C T C A A G C G G	cloned ac 43030 shc
	515	C G G T G G A A T A T C T C A A G C G G	Blast ac shc
	515	C G G T C G A G T A T C T C A A G G C G	cloned at 49025 shc
	518	C G G T C G A G T A T C T C A A G G C G	Blast at shc
40		G A G C A G C G G C C G G A T G G G T G	Majority
		-----+-----+-----	
		550 560	
		-----+-----+-----	
45	538	G A G C A G A A G C C G G A C G G C A G	cloned ac 43030 shc
	535	G A G C A G A A G C C G G A C G G C A G	Blast ac shc
	535	C A A C A A C G C C C A G A T G G G T C	cloned at 49025 shc
	538	C A A C A A C G C C C A G A T G G G T C	Blast at shc
50		C T G G T T T G G T C G C T G G G G C G	Majority
		-----+-----+-----	
		570 580	
		-----+-----+-----	
	558	C T G G T T C G G T C G C T G G G G C G	cloned ac 43030 shc
	555	C T G G T T C G G T C G T T G G G G C G	Blast ac shc
	555	A T G G T T T G G C C G C T G G G G C G	cloned at 49025 shc
55	558	A T G G T T T G G C C G C T G G G G C G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		T C A A C T A C G T G T A T G G C A T G	Majority
		-----+-----	
5		590 600	
		-----+-----	
	578	T C A A C T A C A T C T A C G G C A C G	cloned ac 43030 shc
	575	T C A A T T A C C T C T A C G G C A C G	Blast ac shc
	575	T C A A C T A C G T G T A T G G C A T C	cloned at 49025 shc
10	578	T C A A C T A C G T G T A T G G C A T C	Blast at shc
		G G C G C G G T G G T T T C G G G G C T	Majority
		-----+-----	
		610 620	
		-----+-----	
15	598	G G C G C G G T G G T G T C G G C G C T	cloned ac 43030 shc
	595	G G C G C G G T G G T G T C G G C G C T	Blast ac shc
	595	G G C G C G G T C G T T C C G G G A C T	cloned at 49025 shc
	598	G G C G C G G T C G T T C C G G G A C T	Blast at shc
20		G A A G G C G G T C G G T G T C G A T A	Majority
		-----+-----	
		630 640	
		-----+-----	
25	618	G A A G G C G G T C G G G A T C G A C A	cloned ac 43030 shc
	615	G A A G G C G G T C G G G A T C G A C A	Blast ac shc
	615	C A A G G C C G T C G G T G T C G A T A	cloned at 49025 shc
	618	C A A G G C C G T C G G T G T C G A T A	Blast at shc
30		T G C G T G A G C C G T G G G T T C A A	Majority
		-----+-----	
		650 660	
		-----+-----	
35	638	T G C G C G A G C C G T A C A T T C A A	cloned ac 43030 shc
	635	C G C G C G A G C C G T A C A T T C A A	Blast ac shc
	635	T G C G T G A G C C G T G G G T G C A A	cloned at 49025 shc
	638	T G C G T G A G C C G T G G G T G C A A	Blast at shc
40		A A G T C G C T C G A C T G G G T C G T	Majority
		-----+-----	
		670 680	
		-----+-----	
45	658	A A G G C G C T C G A T T G G G T G G A	cloned ac 43030 shc
	655	A A G G C G C T C G A C T G G G T C G A	Blast ac shc
	655	A A G T C G C T C G A C T G G C T C G T	cloned at 49025 shc
	658	A A G T C G C T C G A C T G G C T C G T	Blast at shc
50		G G A G C A T C A G A A T G C G G A T G	Majority
		-----+-----	
		690 700	
		-----+-----	
	678	G C A G C A T C A G A A C C C G G A C G	cloned ac 43030 shc
	675	G C A G C A T C A G A A C C C G G A C G	Blast ac shc
	675	C G A G C A T C A A A A T G A G G A T G	cloned at 49025 shc
55	678	C G A G C A T C A A A A T G A G G A T G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

```

G C G G C T G G G G T G A A G A C T G - Majority
-----+-----
5          710          720
-----+-----
698 G                               cloned ac 43030 shc
695 G C G G C T G G G G C G A G G A C T G - Blast ac shc
695 G C G G C T G G G G T G A A A G C C G A cloned at 49025 shc
10 698 G C G G T T G G G G T G A A G A T T G - Blast at shc

- - C C G X T C X T A C G A G G A T C C Majority
-----+-----
          730          740
-----+-----
15 698                               cloned ac 43030 shc
714 - - C C G C T C G T A C G A G G A T C C Blast ac shc
715 A T T C C A G C A C A C T G G C G G C C cloned at 49025 shc
717 - - C C G T T C C T A T G A T G A T C C Blast at shc
20

G X X X C T C G C G G G T C A G G G C G Majority
-----+-----
          750          760
-----+-----
25 698                               cloned ac 43030 shc
732 G G C G T A C G C G G G T A A G G G C G Blast ac shc
735 G T T A C T A G T G G A T C C G A G C T cloned at 49025 shc
735 A C G T C T C G C A G G T C A G G G T G Blast at shc

30 C G A G X A C A C C G T C G C A G A C X Majority
-----+-----
          770          780
-----+-----
35 698                               cloned ac 43030 shc
752 C G A G C A C C C C G T C G C A G A C G Blast ac shc
755 C G G T A C C A A G C T T T G G C G T A A cloned at 49025 shc
755 T G A G T A C A C C G T C G C A G A C C Blast at shc

G C C T G G G C G T T G A T G G C G C T Majority
-----+-----
          790          800
-----+-----
40 698                               cloned ac 43030 shc
772 G C C T G G G C G C T G A T G G C G C T Blast ac shc
45 775 T C A T G G T C A T A G C T G T T T C C cloned at 49025 shc
775 G C C T G G G C G T T G A T G G C G C T Blast at shc

C A T C G C G G G C G G C X G T G T C G Majority
-----+-----
          810          820
-----+-----
50 698                               cloned ac 43030 shc
792 C A T C G C G G G C G G C A G G G C G G Blast ac shc
795 T G T G T G A A A T T G - - G T A T C C cloned at 49025 shc
55 795 C A T C G C G G G C G G C C G T G T C G Blast at shc

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Figure 5: Shc polynucleotide sequence alignments (continued)

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5      A G T C A G A X G C C G C A C X X C G C Majority
      -----+-----
              830                      840
      -----+-----

698      cloned ac 43030 shc
812      A G T C C G A G G C C G C G C G C C G C Blast ac shc
813      G C T C A C A A T T C A C A C A A C A T cloned at 49025 shc
10      815      A G T C A G A T G C G G T A T T G C G C Blast at shc

      G G G G T C C X X T A C C T X X X X G - Majority
      -----+-----
              850                      860
      -----+-----

15      698      cloned ac 43030 shc
      832      G G C G T G C A A T A C C T C G T G G - Blast ac shc
      833      A C G A G C C G G A A C A T A A G T G T cloned at 49025 shc
      835      G G G G T C A C T T A C C T T C A C G - Blast at shc

20      A X A C G C A G C G C G C X G A T G - G Majority
      -----+-----
              870                      880
      -----+-----

25      698      cloned ac 43030 shc
      851      A G A C G C A G C G C C C G G A C G - G Blast ac shc
      853      A A G C C T G G G G T G C C T A T G A G cloned at 49025 shc
      854      A C A C G C A G C G C C A G A T G - G Blast at shc

30      T G G C T G X X X Majority
      -----

35      698      cloned ac 43030 shc
      870      C G G C T G G G A Blast ac shc
      873      T G A G C T cloned at 49025 shc
      873      T G G C T G Blast at shc

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Figure 6: Shc amino acid sequence alignments

The degenerate primer range is highlighted red.

5		M T - - - - - E Q L V E A - Majority	
		-----+-----	
		10 20	
		-----+-----	
10	1	M A - - - - - E Q L V E A - A. acidocaldarius ATCC27009	
	1	M A - - - - - E Q L V E A - A. acidocaldarius JCM 5260T	
	1	M T - - - - - K Q L L D T - A. acidoterrestris DSM 3902	
	1	M G T - - - - - Bacillus subtilis	
	1	F T R M T T T N W S L K V D R G R Q T W Dictyostelium discoideum	
	1	M V I A A S - - - - - Synechocystis sp. PCC 6803	
15	1	M T A T T D G S T G A S L R P L A A S - Streptomyces coelicolor A3	
		- - - - - P - - - - - Majority	
		-----+-----	
		30 40	
		-----+-----	
20	9	- - - - - P - - - - - A. acidocaldarius ATCC27009	
	9	- - - - - P - - - - - A. acidocaldarius JCM 5260T	
	9	- - - - - P - - - - - A. acidoterrestris DSM 3902	
	4	- - - - - Bacillus subtilis	
25	21	E Y S Q E K K E A T D V D I H L L R L K Dictyostelium discoideum	
	7	- - - - - Synechocystis sp. PCC 6803	
	20	- - - - - A S D T D I T I - - - - Streptomyces coelicolor A3	
		- - - - - E A V A R Majority	
		-----+-----	
		50 60	
		-----+-----	
35	10	- - - - - A Y A R A. acidocaldarius ATCC27009	
	10	- - - - - A Y A R A. acidocaldarius JCM 5260T	
	10	- - - - - M V Q A A. acidoterrestris DSM 3902	
	4	- - - - - L - - - - - Q E K V R R Bacillus subtilis	
	41	E P G T H C P E G C D L N R A K T P Q Q Dictyostelium discoideum	
	7	- P S V P C P S - - - - - T E Q V R Q Synechocystis sp. PCC 6803	
	28	- P A A A A G V - - - - - P E A A A R Streptomyces coelicolor A3	
40		A L D R A V D Y L L S R Q K A D G Y W W Majority	
		-----+-----	
		70 80	
		-----+-----	
45	14	T L D R A V E Y L L S C Q K D E G Y W W A. acidocaldarius ATCC27009	
	14	T L D R A V E Y L L S C Q K D E G Y W W A. acidocaldarius JCM 5260T	
	14	T L E A G V A H L L R R Q A P D G Y W W A. acidoterrestris DSM 3902	
	11	F Q K K T I T E L R D R Q N A D G S W T Bacillus subtilis	
	61	A I K K A F Q Y F S K V Q T E D G H W A Dictyostelium discoideum	
50	20	A I A A S R D F L L S E Q Y A D G Y W W Synechocystis sp. PCC 6803	
	41	A T R R A T D F L L A K Q D A E G W W K Streptomyces coelicolor A3	

Figure 6: Shc amino acid sequence alignments (continued)

		G P L L S N V T M E A E Y V L L C H I L	Majority
		-----+-----+	
5		90 100	
		-----+-----+	
	34	G P L L S N V T M E A E Y V L L C H I L	A. acidocaldarius ATCC27009
	34	G P L L S N V T M E A E Y V L L C H I L	A. acidocaldarius JCM 5260T
	34	A P L L S N V C M E A E Y V L L C H C L	A. acidoterrestris DSM 3902
10	31	F C F E G P I M T N S F F I L L L T S L	Bacillus subtilis
	81	G D Y G G P M F L L P G L V I T C Y V T	Dictyostelium discoideum
	40	S E L E S N V T I T A E V V I L H K I W	Synechocystis sp. PCC 6803
	61	G D L E T N V T M D A E D L L L R Q F L	Streptomyces coelicolor A3
15		G R V D R E R - - M E K I R R Y L L H E	Majority
		-----+-----+	
		110 120	
		-----+-----+	
	54	D R V D R D R - - M E K I R R Y L L H E	A. acidocaldarius ATCC27009
20	54	D R V D R D R - - M E K I R R Y L L H E	A. acidocaldarius JCM 5260T
	54	G K K N P E R - - E A Q I R K Y I I S Q	A. acidoterrestris DSM 3902
	51	D E G E N E K E L I S S L A A G I H A K	Bacillus subtilis
	101	G Y Q L P E S T Q R E I I R Y L F N R Q	Dictyostelium discoideum
	60	G T A A Q R P - - L E K A K N Y L L Q Q	Synechocystis sp. PCC 6803
25	81	G I Q D E E T - - T R A A A L F I R G E	Streptomyces coelicolor A3
		Q R E D G T W A L Y P G G P - G D L S T	Majority
		-----+-----+	
		130 140	
		-----+-----+	
30	72	Q R E D G T W A L Y P G G P - P D L D T	A. acidocaldarius ATCC27009
	72	Q R E D G T W A L Y P G G P - P D L D T	A. acidocaldarius JCM 5260T
	72	R R E D G T W S I Y P G G P - S D L N A	A. acidoterrestris DSM 3902
	71	Q Q P D G T F I N Y P D E T R G N L T A	Bacillus subtilis
35	121	N P V D G G W G L H I E A H S D I F G T	Dictyostelium discoideum
	78	Q R D H G G W E L Y Y G D G - G E L S T	Synechocystis sp. PCC 6803
	99	Q R E D G T W A T F Y G G P - G E L S T	Streptomyces coelicolor A3
40		T V E A Y V A L K Y L G - V S A D E P H	Majority
		-----+-----+	
		150 160	
		-----+-----+	
	91	T I E A Y V A L K Y I G - M S R D E E P	A. acidocaldarius ATCC27009
	91	T I E A Y V A L K Y I G - M S R D E E P	A. acidocaldarius JCM 5260T
45	91	T V E A Y V A L K Y L G - E P A S D P Q	A. acidoterrestris DSM 3902
	91	T V Q G Y V G M L A S G C F H R T E P H	Bacillus subtilis
	141	T L Q - Y V S L R L L G - V P A D H P S	Dictyostelium discoideum
	97	S V E A Y T A L R I L G - V P A T D P A	Synechocystis sp. PCC 6803
	118	T I E A Y V A L R L A G - D S P E A P H	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		M V K A L E F I Q S Q G G I E S S R V F	Majority
		-----+-----	
5		170 180	
		-----+-----	
	110	M Q K A L R F I Q S Q G G I E S S R V F	A. acidocaldarius ATCC27009
	110	M Q K A L R F I Q S Q G G I E S S R V F	A. acidocaldarius JCM 5260T
	110	M V Q A K E F I Q N E G G I E S T R V F	A. acidoterrestris DSM 3902
10	111	M K K A E Q F I I S H G G L R H V H F M	Bacillus subtilis
	159	V V K A R T F L L Q N G G A T G I P S W	Dictyostelium discoideum
	116	L V K A K N F I V G R G G I S K S R I F	Synechocystis sp. PCC 6803
	137	M A R A A E W I R S R G G I A S A R V F	Streptomyces coelicolor A3
15		T R M W L A L V G E Y P W D K L P M I P	Majority
		-----+-----	
		190 200	
		-----+-----	
	130	T R M W L A L V G E Y P W E K V P M V P	A. acidocaldarius ATCC27009
20	130	T R M W L A L V G E Y P W E K V P M V P	A. acidocaldarius JCM 5260T
	130	T R L W L A M V G Q Y P W D K L P V I P	A. acidoterrestris DSM 3902
	131	T K W M L A A N G L Y P W P A L - Y L P	Bacillus subtilis
	179	G K F W L A T L N A Y D W N G L N P I P	Dictyostelium discoideum
	136	T K M H L A L I G C Y D W R G T P S I P	Synechocystis sp. PCC 6803
25	157	T R I W L A L F G W W K W D D L P E L P	Streptomyces coelicolor A3
		P E I M L L P K N V P L N I Y E F G S W	Majority
		-----+-----	
		210 220	
		-----+-----	
30	150	P E I M F L G K R M P L N I Y E F G S W	A. acidocaldarius ATCC27009
	150	P E I M F L G K R M P L N I Y E F G S W	A. acidocaldarius JCM 5260T
	150	P E I M H L P K S V P L N I Y D F A S W	A. acidoterrestris DSM 3902
	150	L S L M A L P P T L P I H F Y Q F S S Y	Bacillus subtilis
35	199	I E F W L L P Y N L P I A P G R W W C H	Dictyostelium discoideum
	156	P W V M L L P N N F F F N I Y E M S S W	Synechocystis sp. PCC 6803
	177	P E L I Y F P T W V P L N I Y D F G C W	Streptomyces coelicolor A3
40		A R A T V V P L S I V M A Q Q P V - - -	Majority
		-----+-----	
		230 240	
		-----+-----	
	170	A R A T V V A L S I V M S R Q P V - - -	A. acidocaldarius ATCC27009
	170	A R A T V V A L S I V M S R Q P V - - -	A. acidocaldarius JCM 5260T
45	170	A R A T I V T L S Y R H E S P T C - - -	A. acidoterrestris DSM 3902
	170	A R I H F A P M A V T L N Q R - - - -	Bacillus subtilis
	219	C R M V Y L P M S Y I Y A K K T T G P L	Dictyostelium discoideum
	176	A R S S T V P L M I V C D Q K P V - - -	Synechocystis sp. PCC 6803
	197	A R Q T I V P L T I V S A K R P V R P A	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		- F P L P E L A R V P E L Y E T D V P P	Majority
		-----+-----+	
5		250 260	
		-----+-----+	
	187	- F P L P E R A R V P E L Y E T D V P P	A. acidocaldarius ATCC27009
	187	- F P L P E R A R V P E L Y E T D V P P	A. acidocaldarius JCM 5260T
	187	- D A T S G L C K G S G I V R G E G P P	A.acidoterrestris DSM 3902
10	185	- F V L I N R - N I S S L H H L D - - P	Bacillus subtilis
	239	T D L V K D L R R - - E I Y C Q E Y E K	Dictyostelium discoideum
	193	- Y D I A Q G L R V D E L Y A E G M E N	Synechocystis sp. PCC 6803
	217	P F P L D E L H T D P A - - - R P N P P	Streptomyces coelicolor A3
15		R R - R G A K G G G G W - - - I F D A -	Majority
		-----+-----+	
		270 280	
		-----+-----+	
	206	R R - R G A K G G G G W - - - I F D A -	A. acidocaldarius ATCC27009
20	206	R R - R G A K G G G G W - - - I F D A -	A. acidocaldarius JCM 5260T
	206	K R - R S A K G G D S G - - - F F V A -	A.acidoterrestris DSM 3902
	201	H M T K N P F T W L R S - - D A F E E R	Bacillus subtilis
	257	I N W S E Q R N N I S K L D M Y Y E H T	Dictyostelium discoideum
	212	V Q Y K L P E S G T I W - - D I F I G -	Synechocystis sp. PCC 6803
25	234	R P - L A P V A S W D G - - - A F Q R -	Streptomyces coelicolor A3
		- L D S A L H G Y Q K A - - A V H P F R	Majority
		-----+-----+	
		290 300	
		-----+-----+	
30	221	- L D R A L H G Y Q K L - - S V H P F R	A. acidocaldarius ATCC27009
	221	- L D R A L H G Y Q K L - - S V H P F R	A. acidocaldarius JCM 5260T
	221	- L D K F L K A Y N K W - - P I Q P G R	A.acidoterrestris DSM 3902
	219	D L T S I L L H W K R V F H A P F A F Q	Bacillus subtilis
35	277	S L L N V I N G S L N A Y E K V H S K W	Dictyostelium discoideum
	229	- L D S L F K L Q E Q A - - K V V P F R	Synechocystis sp. PCC 6803
	249	- I D K A L H A Y R K V - - A P R R L R	Streptomyces coelicolor A3
40		R A G E A R A L T W I L E R Q E G D G S	Majority
		-----+-----+	
		310 320	
		-----+-----+	
	238	R A A E I R A L D W L L E R Q A G D G S	A. acidocaldarius ATCC27009
	238	R A A E I R A L D W L L E R Q A G D G S	A. acidocaldarius JCM 5260T
45	238	K S G E Q K A L E W I L A H Q E A D G C	A.acidoterrestris DSM 3902
	239	Q L G L Q T A K T Y M L D R I E K D G T	Bacillus subtilis
	297	L R D K A I D Y T F D H I R Y E D E Q T	Dictyostelium discoideum
	246	E Q G L A L A E K W I L E R Q E V S G D	Synechocystis sp. PCC 6803
	266	R A A M N S A A R W I I E R Q E N D G C	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		W G G I Q P P W F Y A L I A L K V L G M	Majority
		-----+-----	
5		330 340	
		-----+-----	
	258	W G G I Q P P W F Y A L I A L K I L D M	A. acidocaldarius ATCC27009
	258	W G G I Q P P W F Y A L I A L K I L D M	A. acidocaldarius JCM 5260T
	258	W G G I Q P P W F Y A L L A L K C L N M	A. acidoterrestris DSM 3902
10	259	L Y S Y A S A T I Y M V Y S L L S L G V	Bacillus subtilis
	317	K Y I D I G P V N K T V N M L C V W D R	Dictyostelium discoideum
	266	W G G I I P A M L N S L L A L K V L G Y	Synechocystis sp. PCC 6803
	286	W G G I Q P P A V Y S V I A L Y L L G Y	Streptomyces coelicolor A3
15		T - Q H P A F I K G L E G L E L Y G V E	Majority
		-----+-----	
		350 360	
		-----+-----	
	278	T - Q H P A F I K G W E G L E L Y G V E	A. acidocaldarius ATCC27009
20	278	T - Q H P A F I K G W E G L E L Y G V E	A. acidocaldarius JCM 5260T
	278	T - D H P A F V K G F E G L E A Y G V H	A. acidoterrestris DSM 3902
	279	S R Y S P I I R R A I T G I K S L V T K	Bacillus subtilis
	337	E G K S P A F Y K H A D R L K D Y - L W	Dictyostelium discoideum
	286	D V N D L Y V Q R G L A A I D N F A V E	Synechocystis sp. PCC 6803
25	306	D L E H P V M R A G L E S L D R F A V W	Streptomyces coelicolor A3
		L S D G G W M F Q A - S I S P V W D T G	Majority
		-----+-----	
		370 380	
		-----+-----	
30	297	L D Y G G W M F Q A - S I S P V W D T G	A. acidocaldarius ATCC27009
	297	L D Y G G W M F Q A - S I S P V W D T G	A. acidocaldarius JCM 5260T
	297	T S D G G W M F Q A - S I S P I W D T G	A. acidoterrestris DSM 3902
	299	C N G I P Y L - E N - S T S T V W D T A	Bacillus subtilis
35	356	L S F D G M K M Q G Y N G S Q L W D T A	Dictyostelium discoideum
	306	T E - D S Y A I Q A - C V S P V W D T A	Synechocystis sp. PCC 6803
	326	R E D G A R M I E A - C Q S P V W D T C	Streptomyces coelicolor A3
40		L A V L A L R A A G L P A D H P A L V K	Majority
		-----+-----	
		390 400	
		-----+-----	
	316	L A V L A L R A A G L P A D H D R L V K	A. acidocaldarius ATCC27009
	316	L A V L A L R A A G L P A D H D R L V K	A. acidocaldarius JCM 5260T
45	316	L T V L A L R S A G L P P D H P A L I K	A. acidoterrestris DSM 3902
	317	L I S Y A L Q K N G V T E T D G S V T K	Bacillus subtilis
	376	F T I Q A F M E S G I A N Q F Q D C M K	Dictyostelium discoideum
	324	W V V R A L A E A D L G K D H P A L V K	Synechocystis sp. PCC 6803
50	345	L A T I A L A D A G V P E D H P Q L V K	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		A G E W L L D R Q I T V P G D W A V K R	Majority
		-----+-----+	
5		410 420	
		-----+-----+	
	336	A G E W L L D R Q I T V P G D W A V K R	A. acidocaldarius ATCC27009
	336	A G E W L L D R Q I T V P G D W A V K R	A. acidocaldarius JCM 5260T
	336	A G E W L V S K Q I L K D G D W K V R R	A. acidoterrestris DSM 3902
10	337	A A D F L L E R Q H T K I A D W S V K N	Bacillus subtilis
	396	L A G H Y L D I S Q V P E D A R D M K H	Dictyostelium discoideum
	344	A G Q W L L D K Q I L T Y G D W Q I K N	Synechocystis sp. PCC 6803
	365	A S D W M L G E Q I V R P G D W S V K R	Streptomyces coelicolor A3
15		- - P N L K P G G W A F E F D N V N Y P	Majority
		-----+-----+	
		430 440	
		-----+-----+	
	356	- - P N L K P G G F A F Q F D N V Y Y P	A. acidocaldarius ATCC27009
20	356	- - P N L K P G G F A F Q F D N V Y Y P	A. acidocaldarius JCM 5260T
	356	- - R K A K P G G W A F E F H C E N Y P	A. acidoterrestris DSM 3902
	357	- - P N S V P G G W G F S N I N T N N P	Bacillus subtilis
	416	Y H R H Y S K G A W P F S T V D H G W P	Dictyostelium discoideum
	364	- - P H G E P G A W A F E F D N N F Y P	Synechocystis sp. PCC 6803
25	385	- - P G L P P G G W A F E F H N D N Y P	Streptomyces coelicolor A3
		D V D D T A V V V - - - L A L N G L R L	Majority
		-----+-----+	
		450 460	
		-----+-----+	
30	374	D V D D T A V V V - - - W A L N T L R L	A. acidocaldarius ATCC27009
	374	D V D D T A V V V - - - W A L N T L R L	A. acidocaldarius JCM 5260T
	374	D V D D T A M V V - - - L A L N G I Q L	A. acidoterrestris DSM 3902
	375	D C D D T T A V L - - - K A I P R N H S	Bacillus subtilis
35	436	I S D C T A E G I K S A L A L R S L P F	Dictyostelium discoideum
	382	D I D D T C V V M - - - M A L Q G I T L	Synechocystis sp. PCC 6803
	403	D I D D T A E V V - - - L A L R R V R H	Streptomyces coelicolor A3
		P D E E R R R D A I T K G F R W L L G M	Majority
		-----+-----+	
		470 480	
		-----+-----+	
40	391	P D E R R R R D A M T K G F R W I V G M	A. acidocaldarius ATCC27009
	391	P D E R R R R D A M T K G F R W I V G M	A. acidocaldarius JCM 5260T
	391	P D E G K R R D A L T R G F R W L R E M	A. acidoterrestris DSM 3902
45	392	P A A W - - - - - E R G V S W L L S M	Bacillus subtilis
	456	I E P I S L D R - I A D G I N V L L T L	Dictyostelium discoideum
	399	P D E E R K Q G A I N K A L Q W I A T M	Synechocystis sp. PCC 6803
	420	H D P E R V E K A I G R G V R W N L G M	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		Q S S N G G W G A Y D V D N T S D L P N	Majority
		-----+-----	
5		490 500	
		-----+-----	
	411	Q S S N G G W G A Y D V D N T S D L P N	A. acidocaldarius ATCC27009
	411	Q S S N G G W G A Y D V D N T S D L P N	A. acidocaldarius JCM 5260T
	411	Q S S N G G W G A Y D V D N T R Q L T K	A. acidoterrestris DSM 3902
10	406	Q N N D G G F S A F E K N V N H P L I R	Bacillus subtilis
	475	Q N G D G G W A S Y E N T R G P K W L E	Dictyostelium discoideum
	419	Q C K T G G W A A F D I D N D Q D W L N	Synechocystis sp. PCC 6803
	440	Q S K N G A W G A F D V D N T S A F P N	Streptomyces coelicolor A3
		H L P - F C D F G E V - I D P P S A D V	Majority
15		-----+-----	
		510 520	
		-----+-----	
	431	H I P - F C D F G E V - T D P P S E D V	A. acidocaldarius ATCC27009
	431	H I P - F C D F G E V - T D P P S E D V	A. acidocaldarius JCM 5260T
20	431	S D S I F A T S G E V - I D P P S E D V	A. acidoterrestris DSM 3902
	426	L L P L E S A E D A A - V D P S T A D L	Bacillus subtilis
	495	K F N P S E V F Q N I M I D Y S Y V E C	Dictyostelium discoideum
	439	Q L P - Y G D L K A M - I D P S T A D I	Synechocystis sp. PCC 6803
	460	R L P - F C D F G E V - I D P P S A D V	Streptomyces coelicolor A3
25		T A H V L E C L G S - - - F G - - - -	Majority
		-----+-----	
		530 540	
		-----+-----	
30	449	T A H V L E C F G S - - - F G - - - -	A. acidocaldarius ATCC27009
	449	T A H V L E C F G S - - - F G - - - -	A. acidocaldarius JCM 5260T
	450	T A H V L E C F G S - - - F G - - - -	A. acidoterrestris DSM 3902
	445	T G R V L H F L G E - - K V G - - - -	Bacillus subtilis
	515	S A A C I Q A M S A F R K H A P N H P R	Dictyostelium discoideum
35	457	T A R V V E M L G A - - - C G - - - -	Synechocystis sp. PCC 6803
	478	T A H V V E M L A V - - - E G - - - -	Streptomyces coelicolor A3
		Y D E A W K V I R R A V E Y L K R E Q E	Majority
		-----+-----	
40		550 560	
		-----+-----	
	461	Y D D A W K V I R R A V E Y L K R E Q K	A. acidocaldarius ATCC27009
	461	Y D D A W K V I R R A V E Y L K R E Q K	A. acidocaldarius JCM 5260T
	462	Y D E A W K V I R K A V E Y L K A Q Q R	A. acidoterrestris DSM 3902
45	458	F T E K H Q H I Q R A V K W L F E H Q E	Bacillus subtilis
	535	I K E I N R S I A R G V K F I K S I Q R	Dictyostelium discoideum
	469	L T M D S P R V E R G L T Y L L Q E Q E	Synechocystis sp. PCC 6803
	490	L A H D P R T - R R G I Q W L L D A Q E	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		Q D G S W F G R W G V N Y L Y G T G A V	Majority
		-----+-----+	
5		570 580	
		-----+-----+	
	481	P D G S W F G R W G V N Y L Y G T G A V	A. acidocaldarius ATCC27009
	481	P D G S W F G R W G V N Y L Y G T G A V	A. acidocaldarius JCM 5260T
	482	P D G S W F G R W G V N Y V Y G I G A V	A.acidoterrestris DSM 3902
10	478	Q N G S W Y G R W G V C Y I Y G T W A A	Bacillus subtilis
	555	Q D G S W L G S W G I C F T Y G T W F G	Dictyostelium discoideum
	489	Q D G S W F G R W G V N Y L Y G T S G A	Synechocystis sp. PCC 6803
	509	T D G S W F G R W G V N Y V Y G T G S V	Streptomyces coelicolor A3
15		V S A L K A V G L D T R E P Y I Q K A L	Majority
		-----+-----+	
		590 600	
		-----+-----+	
	501	V S A L K A V G I D T R E P Y I Q K A L	A. acidocaldarius ATCC27009
20	501	V S A L K A V G I D T R E P Y I Q K A L	A. acidocaldarius JCM 5260T
	502	V P G L K A V G V D M R E P W V Q K S L	A.acidoterrestris DSM 3902
	498	L T G M H A C G L T E S I P V Y K R L C	Bacillus subtilis
	575	I E G L V A S G E P L T S P S I V K A C	Dictyostelium discoideum
	509	L S A L A I Y D A Q R F A P Q I K T A I	Synechocystis sp. PCC 6803
25	529	I P A L T A A G L P T S H P A I R R A V	Streptomyces coelicolor A3
		D W L E S H Q N A D G G W G E D C R S Y	Majority
		-----+-----+	
		610 620	
		-----+-----+	
30	521	D W V E Q H Q N P D G G W G E D C R S Y	A. acidocaldarius ATCC27009
	521	D W V E Q H Q N P D G G W G E D C R S Y	A. acidocaldarius JCM 5260T
	522	D W L V E H Q N E D G G W G E D C R S Y	A.acidoterrestris DSM 3902
	518	V - - - - - - - - - - G S N P Y	Bacillus subtilis
35	595	K F L A S K Q R A D G G W G E S F K S -	Dictyostelium discoideum
	529	A W L L S C Q N A D G G W G E T C E S Y	Synechocystis sp. PCC 6803
	549	R W L E S V Q N E D G G W G E D L R S Y	Streptomyces coelicolor A3
40		E - D P E Y A G Q G A S T A S Q T A W A	Majority
		-----+-----+	
		630 640	
		-----+-----+	
	541	E - D P A Y A G K G A S T P S Q T A W A	A. acidocaldarius ATCC27009
	541	E - D P A Y A G K G A S T P S Q T A W A	A. acidocaldarius JCM 5260T
45	542	D - D P R L A G Q G V S T P S Q T A W A	A.acidoterrestris DSM 3902
	524	K M M T E - A G E N P A K A P K S K - -	Bacillus subtilis
	614	N V T K E Y V Q H E T S Q V V N T G W A	Dictyostelium discoideum
	549	K - N K Q L K G Q G N S T A S Q T A W A	Synechocystis sp. PCC 6803
	569	R Y V R E W S G R G A S T A S Q T G W A	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		L M A L I A G - - - - - G R A E - -	Majority
		-----+-----	
5		650 660	
		-----+-----	
	560	L M A L I A G - - - - - G R A E - -	A. acidocaldarius ATCC27009
	560	L M A L I A G - - - - - G R A E - -	A. acidocaldarius JCM 5260T
	561	L M A L I A G - - - - - G R V E - -	A. acidoterrestris DSM 3902
10	541	- - - - -	Bacillus subtilis
	634	L L S L M S A - K Y P D R - - - - -	Dictyostelium discoideum
	568	L I G L L D A L K Y L P S L G Q D A K L	Synechocystis sp. PCC 6803
	589	L M A L L A A - - - - - G E R D - -	Streptomyces coelicolor A3
15		S E A A E R G V A Y L V E T Q R P D G G	Majority
		-----+-----	
		670 680	
		-----+-----	
	571	S E A A R R G V Q Y L V E T Q R P D G G	A. acidocaldarius ATCC27009
20	571	S E A A R R G V Q Y L V E T Q R P D G G	A. acidocaldarius JCM 5260T
	572	S D A V L R G V T Y L H D T Q R A D G G	A. acidoterrestris DSM 3902
	541	- - - - -	Bacillus subtilis
	646	- E C I E R G I K F L I Q R Q Y P N G D	Dictyostelium discoideum
	588	T T A I E G G V A F L V Q G Q T P K G T	Synechocystis sp. PCC 6803
25	600	S K A V E R G V A W L A A T Q R E D G S	Streptomyces coelicolor A3
		W D E P Y Y T G T G F P G D F Y L G Y T	Majority
		-----+-----	
		690 700	
		-----+-----	
30	591	W D E P Y Y T G T A S P G D F Y L G Y T	A. acidocaldarius ATCC27009
	591	W D E P Y Y T G T G F P G D F Y L G Y T	A. acidocaldarius JCM 5260T
	592	W D E E V Y T G T G F P G D F Y L A Y T	A. acidoterrestris DSM 3902
	541	- - - - -	Bacillus subtilis
35	665	F P Q E S I I G V - F N F N C M I S Y S	Dictyostelium discoideum
	608	W E E A E Y T G T G F P C H F Y I R Y H	Synechocystis sp. PCC 6803
	620	W D E P Y F T G T G F P W D F S I N Y N	Streptomyces coelicolor A3
40		M Y R Q V F P L L A L G R Y K Q A - - -	Majority
		-----+-----	
		710 720	
		-----+-----	
	611	M Y R H V F P T L A L G R Y K Q A - - -	A. acidocaldarius ATCC27009
	611	M Y R H V F P T L A L G R Y K Q A - - -	A. acidocaldarius JCM 5260T
45	612	M Y R D I L P V W A L G R Y Q E A - - -	A. acidoterrestris DSM 3902
	542	M Y R F I - - - - - E E P L	Bacillus subtilis
	684	N Y K N I F P L W A L S R Y N Q - - - L	Dictyostelium discoideum
	628	Y Y R Q Y F P L I A L A R Y S H L Q A -	Synechocystis sp. PCC 6803
	640	L Y R Q V F P L T A L G R Y V H G E P F	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		- - - - - E R - G Majority	
		+-----+	
5		730 740	
		+-----+	
	628	- - - - - I E R R	A. acidocaldarius ATCC27009
	628	- - - - - I E R R	A. acidocaldarius JCM 5260T
	629	- - - - - M Q R I R	A. acidoterrestris DSM 3902
10	551	Y K R P - - - - - G	Bacillus subtilis
	701	Y L K S K - - - - -	Dictyostelium discoideum
	647	- - - - -	Synechocystis sp. PCC 6803
	660	A K K P R A A D A P A E A A P A E V K G	Streptomyces coelicolor A3
15		S Majority	
		--	
		--	
	631		A. acidocaldarius ATCC27009
20	631		A. acidocaldarius JCM 5260T
	634	G	A. acidoterrestris DSM 3902
	556	L	Bacillus subtilis
	706	I	Dictyostelium discoideum
	647	S	Synechocystis sp. PCC 6803
25	680	S	Streptomyces coelicolor A3

Figure 7

1 50
Z.bali sequencing (1) -----TGCATGGCCGTTCTTAGTTGGT
sacc. humal (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
cand. coll (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
grape (1) --CTCTTTCTTGATTTCTATGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
zygo. ruxil (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
PD sequencing (1) ----GTGCTGGAA--TTCGGCT---TTGCATGGCCGTTCTTAGTTGGT
BF sequencing (1) ----TGCCTGGAA--TTCGGCT---TTGCATGGCCGTTCTTAGTTGGT
pen. cry (1) ---TCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
a. nidu (1) AGCTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
euro. amst (1) ----TTCTTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
asp. cand (1) --CTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
chicken (1) --CTCTTTCTCGATTCCGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
wheat (1) --CTCTTTCTTGATCTTATGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
Consensus (1) CTCTTTCTTGAT TT TGG TGGTGGTGCATGGCCGTTCTTAGTTGGT
51 100
Z.bali sequencing (23) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACT
sacc. humal (49) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACT
cand. coll (49) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACT
grape (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
zygo. ruxil (49) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACT
PD sequencing (40) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCCT-T
BF sequencing (39) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCT-T
pen. cry (48) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCCT-T
a. nidu (51) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCCT-T
euro. amst (46) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCCT-T
asp. cand (49) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCCT-T
chicken (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACTCTGGCATGCT
wheat (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
Consensus (51) GGAGTGATTTGTCTGCTTAATTGCGATAACGAACGAGACCTCGGCCCT CT
101 150
Z.bali sequencing (73) AAATAGT--GGTGCTA-GCATTGCTGGTTTTTCCAATTCTTAGAGGGAC
sacc. humal (99) AAATAGT--GGTGCTA-GCATTGCTGGTTAT-CCAATTCTTAGAGGGAC
cand. coll (99) AAATAGT--GGTGCTA-GCATTGCTGGTTAT-CCAATTCTTAGAGGGAC
grape (99) AACTAGCTATGTGAAG-GTGAGCCTCCGCAGC-CAGCTTCTTAGAGGGAC
zygo. ruxil (99) AAATAGT--GGTGCTA-GCATTGCTGGTTTTTCCAATTCTTAGAGGGAC
PD sequencing (89) AAATAGCCCCGGTCC--GCATTGCGGGGCCGC-TGGCTTCTTAGAGGGAC
BF sequencing (88) AAATAGCCCCGGTCC--GCGTTGCGGGGCCGC-TGGCTTCTTAGAGGGAC
pen. cry (97) AAATAGCCCCGGTCC--GCATTGCGGGGCCGC-TGGCTTCTTAGAGGGAC
a. nidu (100) AAATAGCCCCGGTCC--GCGTCCGCGGGGCCGC-TGGCTTCTTAGAGGGAC
euro. amst (95) AAATAGCCCCGGTCC--GCATTGCGGGGCCGC-TGGCTTCTTAGAGGGAC
asp. cand (98) AAATAGCCCCGGTCC--GCATTGCGGGGCCGC-TGGCTTCTTAGAGGGAC
chicken (99) AACTAGCTATGCGGAG-CCATCCCTCCGCAGC-TAGCTTCTTAGAGGGAC
wheat (99) AACTAGCTATGCGGAG-CCATCCCTCCGCAGC-TAGCTTCTTAGAGGGAC
Consensus (101) AAATAGC GGTGC GCATTGCG GGCCGC T GCTTCTTAGAGGGAC

GTGGTGCTAGCATTTGCTG Yeast prime up
CCGCTGGCTTCTTAGGG
Mold prime up

Figure 7 (continued)

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151                                200
Z.bali sequencing (121) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
sacc. humal (145) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
cand. coll (145) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
grape (147) TATGGCCGCTTAGGCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
zygo. ruxil (146) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
PD sequencing (135) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
BF sequencing (134) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
pen. cry (143) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
a. nidu (146) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
euro. amst (141) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
asp. cand (144) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
chicken (149) AAGTGGCGTTTCAGCC-ACCCGAGATTGAG-CAATAACAGGTCTGTGATGC
wheat (147) TATCGCCGTTTAGGCCAGCGAAGTTTGAGGCAATAACAGGTCTGTGATGC
Consensus (151) TATCGGCT CAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC

201                                250
Z.bali sequencing (171) CCTTAGACGTTCTGGGCCCGACGGCGGCTACACTGACGGAGCCAGCGAGT
sacc. humal (195) CCTTAGACGTTCTGGGCCCGACGGCGGCTACACTGACGGAGCCAGCGAGT
cand. coll (195) CCTTAGACGTTCTGGGCCCGACGGCGGCTACACTGACGGAGCCAGCGAGT
grape (197) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGATGTATTCAACGAGT
zygo. ruxil (196) CCTTAGACGTTCTGGGCCCGACGGCGGCTACACTGACGGAGCCAGCGAGT
PD sequencing (184) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACAGGGCCAGCGAGT
BF sequencing (183) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACAGGGCCAGCGGGT
pen. cry (192) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACAGGGCCAGCGAGT
a. nidu (195) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACAGGGCCAGCGAGT
euro. amst (190) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACAGGGCCAGCGAGT
asp. cand (193) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACAGGGCCAGCGAGT
chicken (197) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGACTGGCTCAGCTTGT
wheat (197) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGATGTATTCAACGAGT
Consensus (201) CCTTAGATGTTCTGGGCCCGACGGCGGCTACACTGAC GGGCCAGCGAGT

251                                300
Z.bali sequencing (221) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCTGTGC
sacc. humal (245) CTA-ACCTTGGCCGAGAGGTCTTGGTAATCTTGTGAAACTCCGTCTGTGC
cand. coll (245) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCTGTGC
grape (247) CTATAGCCTTGGGCCGACAGGCCCGGGTAATCTTGTGAAACTCCGTCTGTGA
zygo. ruxil (246) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCTGTGC
PD sequencing (234) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCGTGTCGTGC
BF sequencing (233) ACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGTAAACCCGTGTCGTGC
pen. cry (242) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCGTGTCGTGC
a. nidu (245) ACATCACCTTGGCCGAGAGGCCCGGGTAATCTTGTAAACCCGTGTCGTGC
euro. amst (240) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCGTGTCGTGC
asp. cand (243) ACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGTAAACCCGTGTCGTGC
chicken (247) GTCTACCCCTACGCCGGCAGGCCCGGGTAATCTTGGGAAATTTTCATCGTGA
wheat (247) ATATAGCCCTGGGCCGACAGGCCCGGGTAATCTTGGGAAATTTTCATCGTGA
Consensus (251) ATAT ACCTTGGCCGAGAGGTCTGGGTAATCTTGT AAACCC GTCGTGC

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GGAGCCAGCGAGTCTAAC Yeast primer low
AGGGCCAGCGAGTACATCA Mold primer low
CGGTTTCAAGCCGATGGAAGT Yeast probe
CTCAAGCCGATGGAAGTGCG Mold probe

Figure 7 (continued)

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301                               350
Z.bali sequencing (269) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
sacc. humal (293) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
cand. coll (293) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
grape (296) TGGGGATA-----
zygo. ruxil (294) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
PD sequencing (284) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
BF sequencing (283) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
pen. cry (292) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
a. nidu (295) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
euro. amst (290) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
asp. cand (293) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
chicken (297) TGGGGATCGGGGATTGCAATTATCCCATGAACGAGGAATCCCAGTAA
wheat (297) TGGGGATAGATCATGCAATTGTTGGTCTTCAACGAGGAATGCCTAGTAA
Consensus (301) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTA
351                               400
Z.bali sequencing (319) GCGCAAGTCATCAACTTGCCTTGATTACGTCCCTGCCCTTTGTACACACA
sacc. humal (343) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
cand. coll (343) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
grape (304) -----
zygo. ruxil (344) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
PD sequencing (334) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACA
BF sequencing (333) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACA
pen. cry (342) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
a. nidu (345) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
euro. amst (340) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
asp. cand (343) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
chicken (347) GTGCCGGTCATAAGCTCGCGTTGATTAAAGTCCCTGCCCTTTGTACACACC
wheat (347) GCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCCTTTGTACACACC
Consensus (351) GC CGAGTCATCAGCTCG G GATTACGTCCCTGCCCTTTGTACACACC
401                               450
Z.bali sequencing (369) AGCCGAAT-----
sacc. humal (393) GCGCGTCGCTAG-----
cand. coll (393) GCGCGTCGCTAGTACC-----
grape (304) -----
zygo. ruxil (394) GCGCGTCGCTAGTA-----
PD sequencing (384) AGCCGA--ATT-----
BF sequencing (383) AGCCGA--ATTCTGCAGATA-----
pen. cry (392) GCGCGTCGCTACTACCGATTGAATG-----
a. nidu (395) GCGCGTCGCTAC-----
euro. amst (390) GCGCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCC-----
asp. cand (393) GCGCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCCCTCCGGAAGTGGCT
chicken (397) GCGCGTCGCTA-----
wheat (397) GCGCGTCGCTC-----
Consensus (401) GCGCGTCGCTA

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Alignment 2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
-	A	G	A	G	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	A	A	C	G	C	Consensus	#1																																																																						
.	G A .	G A A	C G C	Consensus	#1																																																																				
-	A	G	A	G	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	A	A	C	G	C	Majority																																																																							

1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	30
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	A	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	G	A	G	-	-	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	
1	G	A	G	A	G	C	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	A	C	G	C	

T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	Consensus #1
T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	.	A	C	A	T	G	C	A	A	G	T	C	G	.	.	Consensus #1
T	G	C	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	Majority

30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	60	
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G	
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
10	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
29	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	A	G
31	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	A	A	C	A	T	G	C	A	A	G	T	C	G	-	-

43030 16S
genbank 16S 43030 AB059664
49029 16S
genbank 16S 49029 AB042059
cc-4902516SRDNA-t7p_C02_006-1-ed
genbank 16S 49025 AB042058
Clostridium elmenteitii
Geobacillus subterraneus 16S AF2
Sulfobacillus disulfidooxidans 1
Bacillus thermoleovorans ribosom

75	- - - - - G C C A G C G G G A C G G G T G	43030 16S
75	- - - - - G C C A G C G G G A C G G G T G	genbank 16S 43030 AB059664
73	- - - - - G T C A G C G G G A C G G G T G	49029 16S
73	- - - - - G T C A G C G G G A C G G G T G	genbank 16S 49029 AB042059
53	- - - - - G C T A G C G G G A C G G G T G	cc-4902516SRDNA-t7p_C02_006-1-ed
73	- - - - - G C T A G C G G G A C G G G T G	genbank 16S 49025 AB042058
90	A A G A G A G G T T A C T T A G C G G G T G	Clostridium elmenteitii
85	- - - - - T T G T C A G C G G G A C G G G T G	Geobacillus subterraneus 16S AF276307
75	- - - - - G T G A G C G G G A C G G G T G	Sulfobacillus disulfidooxidans 16S U349
83	- - - - - T T G T C A G C G G G A C G G G T G	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A G T A A C A C G T G G G C A A T C T G C C . . . C A G A C										Consensus #1
A G . A A C . C G T G G G . A A . C . . . C C										Consensus #1
A G T A A C A C G T G G G C A A T C T G C C T T T C A G A C										Majority
93	A	G	G	A	A	C	A	C	G	43030 16S
93	A	G	G	A	A	C	A	C	G	genbank 16s 43030 AB059664
91	A	G	T	A	A	C	A	C	G	49029 16S
91	A	G	T	A	A	C	A	C	G	genbank 16s 49029 AB042059
71	A	G	T	A	A	C	A	C	G	cc-4902516SRDNA-t7p_C02_006-1-ed
91	A	G	T	A	A	C	A	C	G	genbank 16s 49025 AB042058
120	A	G	T	A	A	C	A	C	G	Clostridium elmenteitii
106	A	G	T	A	A	C	A	C	G	Geobacillus subterraneus 16S AF276307
93	A	G	G	A	A	C	A	C	G	Sulfobacillus disulfidooxidans 16S U349
104	A	G	T	A	A	C	A	C	G	Bacillus thermoleovorans ribosomal RNA

C G G A A T A A C . C C . G G A A A C G G G T G C T A A T G Consensus #1
. G G . A . A A C G G A A A C . . G C T A A . . Consensus #1
C G G A A T A A C G C C C G G A A A C G G G T G C T A A T G Majority

										43030 16S
										genbank 16s 43030 AB059664
										49029 16S
										genbank 16s 49029 AB042059
										cc-4902516SRDNA-t7p_C02_006-1-ed
										genbank 16s 49025 AB042058
										Clostridium elmenteitii
										Geobacillus subterraneus 16S AF276307
										Sulfobacillus disulfidooxidans 16S U349
										Bacillus thermoleovorans ribosomal RNA
123	C	G	G	A	A	T	A	A	C	43030 16S
123	C	G	G	A	A	T	A	A	C	genbank 16s 43030 AB059664
121	C	G	G	A	A	T	A	A	C	49029 16S
121	C	G	G	A	A	T	A	A	C	genbank 16s 49029 AB042059
101	T	G	G	A	A	T	A	A	C	cc-4902516SRDNA-t7p_C02_006-1-ed
121	T	G	G	A	A	T	A	A	C	genbank 16s 49025 AB042058
150	G	G	G	A	A	T	A	A	C	Clostridium elmenteitii
136	C	G	G	A	A	T	A	A	C	Geobacillus subterraneus 16S AF276307
123	T	G	G	A	A	T	A	A	C	Sulfobacillus disulfidooxidans 16S U349
134	C	G	G	A	A	T	A	A	C	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	C	C	G	G	A	T	A	-	-	-	-	C	-	C	G	A	G	-	A	G	G	C	A	T	C	T	-	C	T	T	Consensus #1	
	C	C	-	-	A	T	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	C	-	T	-	-	-	-	-	-	Consensus #1
	C	C	G	G	A	T	A	-	A	C	C	C	G	C	G	A	G	A	G	G	C	A	T	C	T	T	C	T	T	C	T	Majority
	C	C	G	G	A	T	A	-	C	G	C	C	G	C	G	A	G	A	G	G	C	A	T	C	T	C	T	C	T	C	T	43030 16s
	C	C	G	G	A	T	A	-	C	G	C	C	G	C	G	A	G	A	G	G	C	A	T	C	T	C	T	C	T	C	T	genbank 16s 43030 AB059664
	C	C	G	G	A	T	A	-	G	G	C	C	A	G	C	G	A	G	C	A	G	G	A	T	C	T	C	T	C	T	C	49029 16s
	C	C	G	G	A	T	A	-	G	G	C	C	A	G	C	G	A	G	C	A	G	G	A	T	C	T	C	T	C	T	C	genbank 16s 49029 AB042059
	C	C	G	G	A	T	A	-	A	T	A	C	A	C	G	G	T	A	G	G	C	A	T	C	T	C	T	C	T	C	T	cc-4902516SRDNA-t7p_C02_006-1-ed
	C	C	G	G	A	T	A	-	A	T	A	C	A	C	G	G	T	A	G	G	C	A	T	C	T	C	T	C	T	C	T	genbank 16s 49025 AB042058
	C	C	G	G	C	A	T	A	G	C	T	C	T	A	T	A	T	G	G	C	A	T	C	A	T	C	T	C	T	C	T	Clostridium elmenteitii
	C	C	G	G	A	T	A	-	A	C	A	C	A	C	A	G	A	C	C	G	C	A	T	C	T	C	T	C	T	C	T	Geobacillus subterraneus 16S AF276307
	C	C	G	G	A	T	A	-	G	A	C	A	C	A	-	G	A	G	A	G	C	C	T	C	T	C	T	C	T	C	T	Sulfobacillus disulfidooxidans 16S U349
	C	C	G	G	A	T	A	-	A	C	A	C	C	A	C	G	A	G	A	C	C	A	T	C	T	C	T	C	T	C	T	Bacillus thermoleovorans ribosomal RNA

G	.	G	G	.	G	A	A	G	G	T	G	-	C	A	A	.	T	G	-	-	.	A	T	C	G	C	T	G	Consensus #1
.	G	.	A	A	G	G	Consensus #1
G	C	G	G	G	G	A	A	G	G	T	G	-	C	A	A	T	T	G	-	-	C	A	T	C	G	C	T	G	Majority

88

	220										230	240																			
183	G	C	G	G	G	G	G	G	G	G	C	C	-	C	A	A	T	T	G	-	-	G	G	T	G	C	T	G	43030 16s		
183	G	C	G	G	G	G	G	G	G	G	C	C	-	C	A	A	T	T	G	-	-	G	G	C	T	G	C	T	G	genbank 16s 43030 AB059664	
180	G	C	T	G	G	G	G	A	A	G	G	T	G	-	C	A	A	G	T	G	-	-	C	A	C	G	C	A	G	49029 16s	
180	G	C	T	G	G	G	G	A	A	G	G	T	G	-	C	A	A	C	T	G	-	-	C	A	C	G	C	A	G	genbank 16s 49029 AB042059	
160	G	T	G	T	T	G	G	A	A	G	A	T	G	-	C	A	A	C	T	G	-	-	C	A	T	C	G	C	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed
180	G	T	G	T	T	G	G	A	A	G	A	T	G	-	C	A	A	C	T	G	-	-	C	A	T	C	G	C	T	G	genbank 16s 49025 AB042058
210	A	T	A	G	A	G	A	A	A	G	A	T	-	-	T	T	A	T	C	G	-	-	A	T	C	A	-	-	-	-	Clostridium elmenteitii
195	C	G	G	T	T	G	A	A	A	G	G	C	G	C	C	T	T	T	G	G	-	-	C	A	T	C	A	C	T	T	Geobacillus subterraneus 16S AF276307
182	T	G	T	G	G	G	A	A	A	G	A	T	G	-	C	T	A	C	G	G	-	-	C	A	T	C	G	C	C	A	Sulfobacillus disulfidooxidans 16S U34
193	T	G	T	T	G	A	A	A	G	G	C	G	G	C	-	T	T	T	G	G	-	-	G	C	T	G	A	C	T	T	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A . . G A G G A G C C C G C G C G C A T T A G C T A G T T Consensus #1
 . . . G A . G . G C C C G C G . C . . A T T A G C T . G T T Consensus #1
A G G G A G G A G C C C C G C G C G C A T T A G C T A G T T Majority

	250	260	270	
210	A G A G A G A G C C C G C G C G C	A T T A G C C T A G T T	43030 16s	
210	A G A G A G A G C C C G C G C G C	A T T A G C C T A G T T	genbank 16s 43030 AB059664	
207	A T G G A G A G C C C G C G C G C	A T T A G C C T A G T T	49029 16s	
207	A T G G A G A G C C C G C G C G C	A T T A G C C T A G T T	genbank 16s 49029 AB042059	
187	A G A G A G A G C C C G C G C G C	A T T A G C C T A G T T	cc-4902516SRDNA-t7p_C02_006-1-ed	
207	A G A G A G A G C C C G C G C G C	A T T A G C C T A G T T	genbank 16s 49025 AB042058	
233	- - A G A G A G C C C G C G C G C	A T T A G C C T A G T T	Clostridium elmenteitii	
225	G C G G A G A G C C C G C G C G C	A T T A G C C T A G T T	Geobacillus subterraneus 16S AF276307	
209	G T G G A G A G C C C G C G C G C	A T T A G C C T A G T T	Sulfobacillus disulfidooxidans 16S U349	
222	G C G G A G A G C C C G C G C G C	A T T A G C C T A G T T	Bacillus thermoleovorans ribosomal RNA	

G G T G . G G T A A C G G C T C A C C A A G G C G A C G A T Consensus #1
G G . . . G G T A A C G G . . . A C C A A G G C . . . G A T Consensus #1
G G T G G G T A A C G G C T C A C C A A G G C G A C G A T Majority

	280	290	300	
240	G G C G G G T A A C G G C C C	A C C A A G G C G A C	G A T	43030 16s
240	G G C G G G T A A C G G C C C	A C C A A G G C G A C	G A T	genbank 16s 43030 AB059664
237	G G T G G G T A A C G G C C C	A C C A A G G C G A C	G A T	49029 16s
237	G G T G G G T A A C G G C C C	A C C A A G G C G A C	G A T	genbank 16s 49029 AB042059
217	G G T G A G G T A A C G G C C C	A C C A A G G C G A C	G A T	cc-4902516SRDNA-t7p_C02_006-1-ed
237	G G T G A G G T A A C G G C C C	A C C A A G G C G A C	G A T	genbank 16s 49025 AB042058
261	G G T A A G G T A A C G G C C C	A C C A A G G C G A T	G A T	Clostridium elmenteitii
255	G G T A A G G T A A C G G C C C	A C C A A G G C G A T	G A T	Geobacillus subterraneus 16S AF276307
239	G G C G G G T A A C G G C C C	A C C A A G G C G A T	G A T	Sulfobacillus disulfidooxidans 16S U349
252	G G T G A G G T A A C G G C C C	A C C A A G G C G A T	G A T	Bacillus thermoleovorans ribosomal RNA

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Alignment 2

Thursday, September 04, 2003 10:51 AM

G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Consensus #1																														Consensus #1									
. . G T A G C C G . C C T G A G A G G T G . . C G G C C A Consensus #1																														Consensus #1									
G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Majority																														Majority									
270	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	43030 16s									
270	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	genbank 16s 43030 AB059664									
267	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	49029 16s									
267	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	genbank 16s 49029 AB042059									
247	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	cc-4902516SRDNA-t7p_C02_006-1-ed									
267	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	genbank 16s 49025 AB042058									
291	C	A	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	Clostridium elmenteitii									
285	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	Geobacillus subterraneus 16S AF276307									
269	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	Sulfobacillus disulfidooxidans 16S U349									
282	G	C	G	T	A	G	C	C	G	A	C	C	T	G	A	G	A	G	G	T	G	A	C	C	G	G	C	C	A	Bacillus thermoleovorans ribosomal RNA									

C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Consensus #1										Consensus #1									
C A C T G G . A C T G A G A C A C G G . C C A G A C T C C T Consensus #1										Consensus #1									
C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Majority										Majority									

300	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	43030 16S
300	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	genbank 16S 43030 AB059664
297	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	49029 16S
297	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	genbank 16S 49029 AB042059
277	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	cc-4902516SRDNA-t7p_C02_006-1-ed
297	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	genbank 16S 49025 AB042058
321	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Clostridium elmenteitii
315	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Geobacillus subterraneus 16S AF276307
299	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Sulfobacillus disulfidooxidans 16S U34
312	C	A	C	T	G	G	G	A	C	T	G	A	G	A	C	A	C	G	G	C	C	C	A	G	A	C	T	C	C	T	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	A	C	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	C	G	C	A	Consensus #1
	A	C	G	G	A	G	G	C	A	G	C	A	G	T	.	G	G	G	A	A	T	.	T	T	.	C	.	C	A	Consensus #1
	A	C	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	C	G	C	A	Majority

A	T	G	G	G	C	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	Consensus #1	
A	T	G	G	.	.	G	.	A	A	.	.	C	T	G	A	.	G	.	A	G	C	.	A	C	G	C	C	G	C	Consensus #1
A	T	G	G	G	C	C	A	A	G	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	Majority	

360	A	T	G	G	G	C	C	A	A	G	C	C	G	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	43030 16s	
360	A	T	G	G	G	C	C	A	A	G	C	C	G	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	genbank 16s 43030 AB059664
357	A	T	G	G	G	C	C	A	A	G	C	C	G	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	49029 16s
357	A	T	G	G	G	C	C	A	A	G	C	C	G	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	genbank 16s 49029 AB042059
337	A	T	G	G	G	C	C	A	A	G	C	C	G	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	cc-4902516SRDNA-t7p_C02_006-1-ed
357	A	T	G	G	G	C	C	A	A	G	C	C	G	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	genbank 16s 49025 AB042058
381	A	T	G	G	G	G	G	A	A	A	C	C	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	Clostridium elmenteitii
375	A	T	G	G	G	A	A	A	A	A	G	T	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	Geobacillus subterraneus 16S AF276307
359	A	T	G	G	G	C	C	A	A	A	G	C	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	Sulfobacillus disulfidooxidans 16S U34
372	A	T	G	G	G	C	C	A	A	A	G	C	C	C	T	G	A	C	G	G	A	G	C	A	A	C	G	C	C	G	C	Bacillus thermoleovorans ribosomal RNA

Alignment 2

	Consensus #1	Consensus #1	Consensus #1	Majority
G T G A G C G A G A G G C C T T C G G G T T G T A A A G				
G T . A G C G A G A G G C C T T C G G G T . G T A A A G				
G T G A G C G A G A G G C C T T C G G G T T G T A A A G				

390	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
390	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
387	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
387	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
367	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
387	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
411	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450
405	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450
389	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450
402	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450

C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	-	A	G	A	G	C	G	G	C	A	.	G	G	.	G		Consensus #1	
C	T	.	.	G	T	G	G	.	.	G	G	.	.	A	G		Consensus #1
C	T	C	T	G	T	T	G	C	T	C	G	G	G	A	-	A	G	A	G	C	G	G	C	A	A	G	G	G	G		Majority	

	460	470	480	
420	C T G T C T G C T C G G G G - A G A C C G C A T G G G G	43030 16S		
420	G T C T T G C T C G G G G - A G A C C G C A T G G G G	genbank 16S 43030 AB059664		
417	C T C A G T C C T C G G G A - A G A C C G C A A G G G	49029 16S		
417	C T C A G T C C T C G G G A - A G A C C G C A A G G G	genbank 16S 49029 AB042059		
397	C T C T G T T G C T C G G G G - A G A C C A A G G A G	cc-4902516SRDNA-t7p_C02_006-1-ed		
417	C T C T G T T G C T C G G G G - A G A C C A A G G A G	genbank 16S 49025 AB042058		
441	C T C T G T C C T A T G G G A A G A G T - - - -	Clostridium elmenteitii		
435	C T C T G T T G T G A G G G A C G A G C G C G T T	Geobacillus subterraneus 16S AF276307		
419	C T T A G T C A C T C G G G A - A G A C G G - G T G G G A	Sulfobacillus disulfidooxidans 16S U349		
432	C T C T G T T G T G A G G G A C G A G C G C G T T	Bacillus thermoleovorans ribosomal RNA		

Alignment Report of Ali_16S alignment.meg ClustalV (Weighted)

479	G	T	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	43030 16s	
479	G	T	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	genbank 16s 43030 AB059664	
476	G	A	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	49029 16s	
476	G	A	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	genbank 16s 49029 AB042059	
456	G	T	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	cc-4902516SRDNA-t7p_C02_006-1-ed	
476	G	T	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	genbank 16s 49025 AB042058	
476	A	G	A	G	G	A	A	G	C	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	Clostridium elmenteitii	
476	A	G	A	G	G	A	A	G	C	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	Geobacillus subterraneus 16S AF276307	
494	A	C	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G	Sulfobacillus disulfidooxidans 16S U349	
477	G	A	G	A	G	G	A	A	G	C	C	C	C	G	C	A	C	C	C	T	A	C	G	T	G	C	C	A	G	Bacillus thermoleovorans ribosomal RNA	
491	A	C	G	A	G	G	A	A	G	C	C	C	C	G	C	T	A	C	C	T	A	C	G	T	G	C	C	A	G		

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Consensus #1	
	C	A	G	C	C	G	C	G	T	A	A	.	A	C	G	T	A	G	G	G	G	C	.	A	G	C	G	T	Consensus #1	
	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Majority	
	<hr/>																													
509	C	A	G	C	C	G	C	G	T	A	A	A	A	C	G	T	A	G	G	G	G	C	G	A	G	C	G	T	43030 16s	
509	C	A	G	C	C	G	C	G	T	A	A	A	A	A	C	G	T	A	G	G	G	G	C	G	A	G	C	G	T	genbank 16s 43030 AB059664
506	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	49029 16s	
506	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	genbank 16s 49029 AB042059	
486	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	cc-4902516SRDNA-t7p_C02_006-1-ed	
506	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	genbank 16s 49025 AB042058	
506	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Clostridium elmenteitii	
506	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Geobacillus subterraneus 16S AF276307	
524	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Sulfobacillus disulfidooxidans 16S U349	
507	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T	Bacillus thermoleovorans ribosomal RNA	
521	C	A	G	C	C	G	C	G	T	A	A	T	A	C	G	T	A	G	G	G	G	C	A	A	G	C	G	T		

T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Consensus #1	
T	.	T	C	C	G	G	A	A	T	.	A	.	T	G	G	G	.	C	G	T	A	A	A	G	.	G	.	G	C	Consensus #1
T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Majority

539	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	G	T	G	C	43030 16S	
539	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	G	T	G	C	genbank 16S 43030 AB059664	
536	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	T	G	C	49029 16S	
536	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	T	G	C	genbank 16S 49029 AB042059	
516	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	G	G	C	G	T	A	A	A	G	C	T	G	C	cc-4902516SRDNA-t7p_C02_006-1-ed
536	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	T	G	C	genbank 16S 49025 AB042058	
536	T	A	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	G	T	G	C	Clostridium elmenteitii	
554	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Geobacillus subterraneus 16S AF276307
537	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	G	T	G	C	Sulfobacillus disulfidooxidans 16S U349	
551	T	G	T	C	C	G	G	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

G T A G G C G G T T G . G T A A G T C T G . . G T G A A A G Consensus #1										G T G A A A G Consensus #1										
G . A . G C G G G T C . G . . . T G A A A G Consensus #1										G T G A A A G Consensus #1										
G T A G G C G G T T G C G T A A G T C T G G G G T G A A A G Majority										G T G A A A G Majority										
568	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										43030 16s									
568	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										genbank 16s 43030 AB059664									
565	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										49029 16s									
565	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										genbank 16s 49029 AB042059									
546	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										cc-4902516SRDNA-t7p_C02_006-1-ed									
565	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										genbank 16s 49025 AB042058									
565	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										Clostridium elmenteitii									
583	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										Geobacillus subterraneus 16S AF276307									
566	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										Sulfobacillus disulfidooxidans 16S U349									
580	G T A G G C G G T T G C G T A A G T C T G . . G T G A A A G										Bacillus thermoleovorans ribosomal RNA									
T C C A . G G C T C A A C C . T G G G A . . G C . T T G G A Consensus #1										Consensus #1										
. . . . G G C T C . A C C . T C . T T . G A Consensus #1										Consensus #1										
T C C A G G G C T C A A C C G T G G G A A T G C T T T G G A Majority										Majority										
598	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										43030 16s									
598	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										genbank 16s 43030 AB059664									
595	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										49029 16s									
595	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										genbank 16s 49029 AB042059									
576	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										cc-4902516SRDNA-t7p_C02_006-1-ed									
595	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										genbank 16s 49025 AB042058									
595	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										Clostridium elmenteitii									
595	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										Geobacillus subterraneus 16S AF276307									
613	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										Sulfobacillus disulfidooxidans 16S U349									
596	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A										Bacillus thermoleovorans ribosomal RNA									
610	T C C A T G G C T C A A C C C A T G G G A T G G G A T G G A																			

Alignment 2

Alignment Report of Ali_16S_aligment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A A C T G C . T G - A C T T G A G T G C T G G A G A G G C A Consensus #1
 A A C T G C T T G A G T G C . G G A G A G G . . Consensus #1
 A A C T G C G T G - A C T T G A G T G C T G G A G A G G C A Majority

628	A A C T G C	T G - A	C T T G A G T G C T G G A G A G G C A	43030 16s
628	A A C T G C	T G - A	C T T G A G T G C T G G A G A G G C A	genbank 16s 43030 AB059664
625	A A C T G C	T A - A	C T T G A G T G C T G G A G A G G C A	49029 16s
625	A A C T G C	T A - A	C T T G A G T G C T G G A G A G G C A	genbank 16s 49029 AB042059
606	A A C T G C	T G A	C T T G A G T G C T G G A G A G G C N	cc-4902516SRDNA-t7p_C02_006-1-ed
625	A A C T G C	T G - A	C T T G A G T G C T G G A G A G G C A	genbank 16s 49025 AB042058
624	A A C T G C	T A G -	C T T G A G T G C T G G A G A G G T A	Clostridium elmenteitii
643	A A C T G C	T G G A	C T T G A G T G C T G G A G A G G A G	Geobacillus subterraneus 16S AF276307
626	A A C T G C	T A G -	C T T G A G T G C T G G A G A G G C A	Sulfobacillus disulfidooxidans 16S U349
640	A A C T G C	T G G A	C T T G A G T G C T G G A G A G G A G	Bacillus thermoleovorans ribosomal RNA

A G G G G A A T T C C A C G T G T - A G C G G T G . A A - T Consensus #1
 A G . . . A A T T C C . . G T G T . A . C G G T G . A A . T Consensus #1
 A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T Majority

657	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A - T	43030 16s
657	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	genbank 16s 43030 AB059664
654	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	49029 16s
654	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	genbank 16s 49029 AB042059
636	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	cc-4902516SRDNA-t7p_C02_006-1-ed
654	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	genbank 16s 49025 AB042058
653	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	Clostridium elmenteitii
672	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	Geobacillus subterraneus 16S AF276307
655	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	Sulfobacillus disulfidooxidans 16S U349
669	A G G G G A	T T C C A	C G T G T -	A G C G G T G .	A A . T	Bacillus thermoleovorans ribosomal RNA

Alignment Report of Ali 16S alignment.meq ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	730	740	750	
G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C				Consensus #1
G C G . . A . A . A T . . G G A G G A A . A C C A G T G G C				Consensus #1
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C				Majority
G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C				43030 16s
G C G T - A G A G A G A T G T G G A G G A A T A C C A G T G G C				genbank 16s 43030 AB059664
G C G T - A G A G A G A T G T G G A G G A A T A C C A G T G G C				49029 16s
G C G T - A G A G A G A T G T G G A G G A A T A C C A G T G G C				genbank 16s 49029 AB042059
G C G N T A N A T G T G G A G G A A T A C C A G T G G C				cc-4902516SRDNA-t7p_C02_006-1-ed
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C				genbank 16s 49025 AB042058
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C				Clostridium elmenteitii
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C				Geobacillus subterraneus 16S AF276307
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C				Sulfobacillus disulfidooxidans 16S U349
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C				Bacillus thermoleovorans ribosomal RNA

G	A	A	G	C	C	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G		Consensus #1
.	A	A	.	G	C	G	.	C	T	.	.	C	T	G	G	.	C	.	G	Consensus #1
G	A	A	G	C	C	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G		Majority

714	G	A	A	R	G	G	G	C	C	T	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	43030 16S	
714	G	A	A	G	G	G	G	C	C	T	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	genbank 16S 43030 AB059664	
711	G	A	A	G	G	G	G	C	C	T	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	49029 16S	
711	G	A	A	G	G	G	G	C	C	T	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	genbank 16S 49029 AB042059	
696	N	A	A	N	G	G	G	C	C	T	T	T	G	C	T	G	G	A	C	A	G	T	G	G	-	-	-	-	-	-	A	cc-4902516SRDNA-t7p_C02_006-1-ed
711	G	A	A	G	G	G	G	C	C	T	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	genbank 16S 49025 AB042058	
710	G	A	A	G	G	G	G	A	C	T	T	-	A	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	Clostridium elmenteitii	
729	G	A	A	G	G	G	G	G	C	T	T	C	T	-	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	Geobacillus subterraneus 16S AF276307
712	G	A	A	G	G	G	G	C	C	T	T	-	G	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	Sulfobacillus disulfidooxidans 16S U349	
726	G	A	A	G	G	G	G	G	C	T	T	C	T	-	C	T	G	G	A	C	A	G	T	G	A	C	T	G	A	C	G	Bacillus thermoleovorans ribosomal RNA

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C T G A G G C A C G A A A G C G T G G G A G C A A A C A G										Consensus #1	
C T G A										Consensus #1	
C T G A G G C A C G A A A G C G T G G G A G C A A A C A G										Majority	
743	C	T	G	A	G	G	C	A	C	G	43030 16s
743	G	G	C	A	C	G	A	A	G	C	genbank 16s 43030 AB059664
740	G	G	C	A	C	G	A	A	G	C	49029 16s
740	G	G	C	A	C	G	A	A	G	C	genbank 16s 49029 AB042059
721	C	T	G	A	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
740	C	T	G	A	G	G	C	A	A	G	genbank 16s 49025 AB042058
739	C	T	G	A	G	G	C	A	C	G	Clostridium elmenteitii
758	C	T	G	A	G	G	C	A	C	G	Geobacillus subterraneus 16S AF276307
741	C	T	G	A	G	G	C	A	C	G	Sulfobacillus disulfidooxidans 16S U349
755	C	T	G	A	G	G	C	A	C	G	Bacillus thermoleovorans ribosomal RNA
G A T T A G A T A C C C T G G T A G T C C A C G C C G T A A										Consensus #1	
.										Consensus #1	
G A T T A G A T A C C C T G G T A G T C C A C G C C G T A A										Majority	
773	G	A	T	T	A	G	A	T	A	C	43030 16s
773	G	A	T	T	A	G	A	T	A	C	genbank 16s 43030 AB059664
770	G	A	T	T	A	G	A	T	A	C	49029 16s
770	G	A	T	T	A	G	A	T	A	C	genbank 16s 49029 AB042059
725	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
770	G	A	T	T	A	G	A	T	A	C	genbank 16s 49025 AB042058
768	G	A	T	T	A	G	A	T	A	C	Clostridium elmenteitii
788	G	A	T	T	A	G	A	T	A	C	Geobacillus subterraneus 16S AF276307
771	G	A	T	T	A	G	A	T	A	C	Sulfobacillus disulfidooxidans 16S U349
784	G	A	T	T	A	G	A	T	A	C	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	Consensus #1	
.	Consensus #1	
A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	T	G	G	-	G	G	G	T	C	A	C	Majority

850 860 870

803	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	43030 16S
803	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	genbank 16S 43030 AB059664
800	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	49029 16S
800	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	genbank 16S 49029 AB042059
725	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
800	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	genbank 16S 49025 AB042058
798	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	Clostridium elmenteitii
818	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	Geobacillus subterraneus 16S AF276307
801	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	Sulfobacillus disulfidooxidans 16S U349
814	A	C	G	A	T	G	A	G	T	G	C	T	A	G	G	T	G	T	G	G	-	G	G	G	T	C	A	C	Bacillus thermoleovorans ribosomal RNA

A	C	C	C	.	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	C	C	C	A	A	T	A	A	G	Consensus #1	
.	Consensus #1	
A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	C	C	C	A	A	T	A	A	G	Majority

880 890 900

832	A	C	C	C	-	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	M	C	C	A	A	T	A	A	G	43030 16S	
832	A	C	C	C	-	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	C	C	C	A	A	T	A	A	G	genbank 16S 43030 AB059664	
829	A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	C	C	C	A	A	T	A	A	G	49029 16S	
829	A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	C	C	C	A	A	T	A	A	G	genbank 16S 49029 AB042059	
725	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
829	A	C	C	C	-	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	C	C	C	A	A	T	A	A	G	genbank 16S 49025 AB042058	
826	A	C	C	-	-	-	-	T	C	A	G	T	G	C	C	G	A	G	C	A	A	C	C	C	A	A	T	A	A	G	Clostridium elmenteitii	
848	A	C	C	C	T	T	T	A	G	T	G	C	C	G	A	G	G	C	T	A	A	C	C	C	G	A	T	A	A	G	Geobacillus subterraneus 16S AF276307	
830	A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	A	C	C	C	C	A	A	T	A	A	G	Sulfobacillus disulfidooxidans 16S U349
844	A	C	C	C	T	T	T	A	G	T	G	C	C	G	A	G	G	-	T	A	A	C	G	C	G	A	T	A	A	G	Bacillus thermoleovorans ribosomal RNA	

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	910	920	930	Consensus #1
860	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			43030 16s
860			genbank 16s 43030 AB059664
858	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			49029 16s
858	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			genbank 16s 49029 AB042059
734	- - - - -			cc-4902516SRDNA-t7p_C02_006-1-ed
857	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			genbank 16s 49025 AB042058
854	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			Clostridium elmentarii
878	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			Geobacillus subterraneus 16S AF276307
859	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			Sulfobacillus disulfidooxidans 16S U349
873	C A C T C C G C C T G G G G A G T A C G G T C G C A A G A C			Bacillus thermoleovorans ribosomal RNA

	940	950	960	Consensus #1
890	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			43030 16s
890			genbank 16s 43030 AB059664
888	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			49029 16s
888	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			genbank 16s 49029 AB042059
734	- - - - -			cc-4902516SRDNA-t7p_C02_006-1-ed
887	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			genbank 16s 49025 AB042058
884	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			Clostridium elmentarii
908	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			Geobacillus subterraneus 16S AF276307
889	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			Sulfobacillus disulfidooxidans 16S U349
903	T G A A A C T C A A A G G A A T T G A C G G G G G - C C C G			Bacillus thermoleovorans ribosomal RNA

Alignment 2

	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	Consensus #1
	Consensus #1
	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	Majority

	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	43030 16s
919	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	genbank 16s 43030 AB059664
919	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	49029 16s
917	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	genbank 16s 49029 AB042059
917	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	cc-4902516SRDNA-t7p_C02_006-1-ed
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	genbank 16s 49025 AB042058	
916	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	Clostridium elmenteitii
914	C	A	C	A	G	C	A	G	[C]	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	Geobacillus subterraneus 16S AF276307
937	C	A	C	A	G	C	[G]	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	Sulfobacillus disulfidooxidans 16S U349
918	C	A	C	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	Bacillus thermoleovorans ribosomal RNA
932	C	A	C	A	G	C	[G]	G	T	G	G	A	G	C	A	T	G	T	T	A	A	T	T	C	G	

	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Consensus #1
	Consensus #1	
	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Majority

	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	43030 16s
949	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 43030 AB059664
949	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	49029 16s
947	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	N	C	A	G	G	C	T	C	G	genbank 16s 49029 AB042059
947	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	genbank 16s 49025 AB042058	
946	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Clostridium elmenteitii
944	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	[T]G	A	G	C	T	T	G	Geobacillus subterraneus 16S AF276307
967	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Sulfobacillus disulfidooxidans 16S U34
948	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Bacillus thermoleovorans ribosomal RNA
962	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

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A	C	A	T	C	C	C	.	C	T	G	A	C	A	.	C	C	.	A	G	A	G	A	T	-	-	-	G	C		Consensus #1
.	Consensus #1
A	C	A	T	C	C	C	T	C	T	G	A	C	A	G	C	C	G	C	A	G	A	G	A	T	-	-	-	G	C	Majority

	1030	1040	1050	
979	A C A T C C C T C T G A C A C C C T C C A G A T - - - G A	43030 16s		
979	A C A T C C C T C T G A C A C C C T C C A G A T - - - G A	genbank 16s 43030 AB059664		
977	A C A T C C C C C T G A C A G C C G C A G A T - - - G C	49029 16s		
977	A C A T C C C C C T G A C A G C C G C A G A T - - - G C	genbank 16s 49029 AB042059		
744	- -	cc-4902516SRDNA-t7p_C02_006-1-ed		
976	A C A T C C C T C T G A C C G G T G C A G A G A T - - - G T	genbank 16s 49025 AB042058		
974	A C A T C C C T C T G A C C G G T G A G T A A A - - - G T C	Clostridium elmenteitii		
997	A C A T C C C C - C T G A C A A C C C A A G A G A T T G G G C C	Geobacillus subterraneus 16S AF2		
978	A C A T C C C C C A G A C G G G T G T A G A G A T - - - A C	Sulfobacillus disulfidooxidans 1		
992	A C A T C C C C - C T G A C A A C C C A A G A G A T T G G G C C	Bacillus thermoleovorans ribosom		

G	.	.	T	C	C	C	T	T	C	G	G	G	C	A	G	-	-	.	G	G	A	G	A	C	A	G	G	Consensus #1
.	Consensus #1
G	G	T	T	T	C	C	C	T	T	C	G	G	G	C	A	G	-	-	G	G	G	A	G	A	C	A	G	Majority

	1060	1070	1080	
1006	G G G T C C C T T C G G G G C A G - -	A G G A G A C A G G	43030 16S	
1006	G G G T C C C T T C G G G G C A G - -	A G G A G A C A G G	genbank 16S 43030 AB059664	
1004	G T T T C C C T T C G G G G C A G - -	G G G A G A C A G G	49029 16S	
1004	G G T T T C C C T T C G G G G C A G - -	G G G A G A C A G G	genbank 16S 49029 AB042059	
744	- - - - - - - - - - - - - - - -	- - - - - - - - - - - - - - - -	cc-4902516SRDNA-t7p_C02_006-1-ed	
1003	A C C T T C C C T T C G G G G C A G - -	A G G A G A C A G G	genbank 16S 49025 AB042058	
1001	A C C T T C C C T T C G G G A C A G - -	A G G A G A C A G G	Clostridium elmenteitii	
1026	G T C C C C T T C G G G G G A C A G - -	G G G T G A C A G G	Geobacillus subterraneus 16S AF2	
1005	A C C T C C C T T C G G G G C T G - -	G G G A G A C A G G	Sulfobacillus disulfidooxidans 1	
1021	G T C C T T C - - - - G G G G G A C A G - -	G G G T G A C A G G	Bacillus thermovorans ribosom	

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Alignment 2

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	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	C	G	T	Consensus #1		
	Consensus #1		
	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	C	G	T	Majority		
	1090										1100										1110										
1034	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	43030 16s
1034	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	genbank 16s 43030 AB059664
1032	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	49029 16s
1032	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	genbank 16s 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1031	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	genbank 16s 49025 AB042058
1029	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Clostridium elmenteitii
1056	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Geobacillus subterraneus 16S AF276307
1033	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Sulfobacillus disulfidooxidans 16S U349
1047	T	G	G	T	G	C	A	T	G	G	T	T	G	T	C	G	T	C	A	G	C	T	C	G	T	G	T	C	G	T	Bacillus thermoleovorans ribosomal RNA
	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Consensus #1
	Consensus #1	
	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Majority
	1120										1130										1140										
1064	G	A	G	A	T	G	T	T	G	G	G	T	T	C	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	43030 16s
1064	G	A	G	A	T	G	T	T	G	G	G	T	T	C	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	genbank 16s 43030 AB059664
1062	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	49029 16s
1062	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	genbank 16s 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1061	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	genbank 16s 49025 AB042058
1059	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Clostridium elmenteitii
1086	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Geobacillus subterraneus 16S AF276307
1063	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	A	G	C	G	Sulfobacillus disulfidooxidans 16S U349
1077	G	A	G	A	T	G	T	T	G	G	G	T	T	A	A	G	T	C	C	C	G	C	A	A	C	G	C	G	C	G	Bacillus thermoleovorans ribosomal RNA

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	C	A	A	C	C	C	T	T	G	A	.	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	.	Consensus #1	
	Consensus #1	
	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	T	A	Majority
	1150										1160										1170										
1094	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	T	G	43030 16s
1094	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	T	G	genbank 16s 43030 AB059664
1092	C	A	A	C	C	C	T	T	G	A	A	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	G	A	49029 16s
1092	C	A	A	C	C	C	T	T	G	A	A	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	G	A	genbank 16s 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1091	C	A	A	C	C	C	T	T	G	A	T	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	A	G	genbank 16s 49025 AB042058
1089	C	A	A	C	C	C	T	T	G	A	T	C	A	T	G	T	T	G	C	C	A	G	C	A	T	-	T	T	C		Clostridium elmenteitii
1116	C	A	A	C	C	C	T	T	G	A	C	T	C	T	A	G	T	T	G	C	C	A	G	C	A	T	-	-	C		Geobacillus subterraneus 16S AF276307
1093	C	A	A	C	C	C	T	T	G	A	T	C	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	A	A		Sulfobacillus disulfidooxidans 16S U349
1107	C	A	A	C	C	C	T	T	G	A	C	T	C	T	A	G	T	T	G	C	C	A	G	C	A	C	G	-	-	A	Bacillus thermoleovorans ribosomal RNA
	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	Consensus #1
	.	.	.	G	G	G	.	A	Consensus #1	
	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	Majority
	1180										1190										1200										
1124	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	43030 16s
1124	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16s 43030 AB059664
1122	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	T	T	G	A	C	T	G	C	C	G	G	C	G	-	49029 16s
1122	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	T	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16s 49029 AB042059
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1121	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16s 49025 AB042058
1118	G	G	A	T	G	G	G	C	A	C	T	C	T	A	A	T	G	A	C	T	G	C	C	G	G	T	G	A			Clostridium elmenteitii
1144	A	G	T	T	G	G	G	C	A	C	T	C	T	A	G	A	G	G	A	C	T	G	C	C	G	G	C	G	A		Geobacillus subterraneus 16S AF276307
1123	A	G	G	C	G	G	G	G	A	C	T	C	A	C	C	G	G	T	G	A	C	T	G	C	C	G	T	C	G	-	Sulfobacillus disulfidooxidans 16S U349
1135	A	G	G	T	G	G	G	C	A	C	T	C	T	A	G	A	G	G	A	C	T	G	C	C	G	T	G	A			Bacillus thermoleovorans ribosomal RNA

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T A A G T C G G A G G A A G G C G G G G A T G A C G T C A A										Consensus #1
.										Consensus #1
T A A G T C G G A G G A A G G C G G G G A T G A C G T C A A										Majority
1153	T	A	A	G	T	C	G	G	A	43030 16s
1153	T	A	A	G	T	C	G	G	A	genbank 16s 43030 AB059664
1151	T	A	A	G	T	C	G	G	A	49029 16s
1151	T	A	A	G	T	C	G	G	A	genbank 16s 49029 AB042059
752	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1150	T	A	A	G	T	C	G	G	A	genbank 16s 49025 AB042058
1148	C	A	A	C	G	G	A	A	G	Clostridium elmenteitii
1174	A	A	G	T	C	G	G	A	A	Geobacillus subterraneus 16S AF276307
1152	T	A	A	G	A	C	G	G	A	Sulfobacillus disulfidooxidans 16S U349
1165	C	A	A	G	T	C	G	G	A	Bacillus thermoleovorans ribosomal RNA
A T C A T C A T G C C C C T T A T G T C C T G G G C T A C A										Consensus #1
.										Consensus #1
A T C A T C A T G C C C C T T A T G T C C C T G G G C T A C A										Majority
1183	A	T	C	A	T	C	A	T	G	43030 16s
1183	A	T	C	A	T	C	A	T	G	genbank 16s 43030 AB059664
1181	A	T	C	A	T	C	A	T	G	49029 16s
1181	A	T	C	A	T	C	A	T	G	genbank 16s 49029 AB042059
752	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1180	A	T	C	A	T	C	A	T	G	genbank 16s 49025 AB042058
1178	A	T	C	A	T	C	A	T	G	Clostridium elmenteitii
1204	A	T	C	A	T	C	A	T	G	Geobacillus subterraneus 16S AF276307
1182	A	T	C	A	T	C	A	T	G	Sulfobacillus disulfidooxidans 16S U349
1195	A	T	C	A	T	C	A	T	G	Bacillus thermoleovorans ribosomal RNA

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C A C G T G C T A C A A T G G G C G G T A C A A . G G G A .																				Consensus #1																			
.																				Consensus #1																			
C A C G T G C T A C A A T G G G C G G T A C A A C G G G A A																				Majority																			
1270										1280										1290																			
1213	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	G	G	G	A	G	43030 16s												
1213	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	G	G	G	A	G	genbank 16s 43030 AB059664												
1211	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	G	G	A	A	49029 16s												
1211	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	G	G	A	A	genbank 16s 49029 AB042059												
752	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	N	G	G	A	-	cc-4902516SRDNA-t7p_C02_006-1-ed												
1210	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	G	G	A	A	genbank 16s 49025 AB042058												
1208	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	C	G	A	A	A	A	G	G	G	C	A	Clostridium elmenteitii												
1234	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	A	G	G	G	C	T	Geobacillus subterraneus 16S AF276307											
1212	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	G	G	G	A	C	Sulfobacillus disulfidooxidans 16S U349											
1225	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	A	G	G	G	C	T	Bacillus thermoleovorans ribosomal RNA											
G C G A A . C C G C G A G G . G G A G C . A A . C C C A . A																				Consensus #1																			
.																				Consensus #1																			
G C G A A G C C G C G A G G T G G A G C G A A C C C C A A A																				Majority																			
1300										1310										1320																			
1243	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	G	A	G	C	A	A	A	C	C	C	A	A	43030 16s											
1243	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	G	A	G	C	A	A	A	C	C	C	A	A	genbank 16s 43030 AB059664											
1241	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	A	A	C	C	C	C	A	A	C	C	C	T	G	49029 16s										
1241	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	A	A	C	C	C	C	A	A	C	C	C	T	G	genbank 16s 49029 AB042059										
760	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed												
1240	G	C	G	A	A	G	C	C	G	C	G	A	G	G	T	G	A	G	C	A	A	A	C	C	T	A	A	genbank 16s 49025 AB042058											
1238	G	C	G	A	A	G	C	C	G	A	A	T	C	C	G	A	A	C	C	C	C	A	T	A	A	A	A	Clostridium elmenteitii											
1264	G	C	G	A	A	C	C	G	C	G	A	G	G	G	G	A	G	C	A	T	C	C	C	C	A	A	A	Geobacillus subterraneus 16S AF276307											
1242	G	C	G	A	A	G	C	C	G	A	A	T	C	T	G	A	G	C	A	A	C	C	C	C	T	G	A	Sulfobacillus disulfidooxidans 16S U349											
1255	G	C	G	A	A	C	C	G	C	G	A	G	G	G	G	A	G	C	A	T	C	C	C	C	A	A	A	Bacillus thermoleovorans ribosomal RNA											

Alignment 2

Thursday, September 04, 2003 10:51 AM

AAGCCG	.TCGTAGTTCTCGGATTTGCAGGCTTG	C		Consensus #1
.....TT.....	.		Consensus #1
AAGCCGCTCCTAGTTCGGATTTCACAGGCTGC				Majority

1273	AAGCCGCTCCTAGTTCGGATTTCGAGGCTTG	43030 16s
1273	AAGCCGCTCCTAGTTCGGATTTCGAGGCTTG	genbank 16s 43030 AB059664
1271	AAGCCGCTCCTAGTTCGGATTTCGAGGCTTG	49029 16s
1271	AAGCCGCTCCTAGTTCGGATTTCGAGGCTTG	genbank 16s 49029 AB042059
760	- - - - -	cc-4902516SRDNA-t7p_C02_006-1-ed
1270	AAGCCGCTCCTAGTTCGGATTTCGAGGCTTG	genbank 16s 49025 AB042058
1268	AAGTCGGTCCAGTTCGGATTTCGAGGCTTG	Clostridium elmenteitii
1294	AAGCCGCTCCTAGTTCGGATTTCGAGGCTTG	Geobacillus subterraneus 16S AF276307
1272	AAACC GCTCCTAGTTCGGATTTCGAGGCTTG	Sulfobacillus disulfidooxidans 16S U349
1285	AAGCCGCTCTCAGTTCGGATTTCGAGGCTTG	Bacillus thermoleovorans ribosomal RNA

AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	C		Consensus #1
.....		Consensus #1
AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG			Majority

1303	AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	43030 16s
1303	AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	genbank 16s 43030 AB059664
1301	AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	49029 16s
1301	AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	genbank 16s 49029 AB042059
765	- - - - -		cc-4902516SRDNA-t7p_C02_006-1-ed
1300	AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	genbank 16s 49025 AB042058
1298	AAC	TCCGCTGCCATGAGTAGTGGAGTTCGCTAG	Clostridium elmenteitii
1324	AAC	TCCGCTGCA TG A AGCCGGA AT C GCTAG	Geobacillus subterraneus 16S AF276307
1302	AAC	TCCGCTGCA TG A AGCCGGA AT TGC TAG	Sulfobacillus disulfidooxidans 16S U349
1315	AAC	TCCGCTGCA TG A AGCCGGA AT C GCTAG	Bacillus thermoleovorans ribosomal RNA

Thursday, September 04, 2003 10:51 AM

T A A T C G C G G A T C A G C A T G C C G C G G T G A A T .																										Consensus #1																			
.																										Consensus #1																			
T A A T C G C G G A T C A G C A T G C C G C G G T G A A T C																										Majority																			
1390													1400													1410																			
1333	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	43030 16s														
1333	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	genbank 16s 43030 AB059664														
1331	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	49029 16s														
1331	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	genbank 16s 49029 AB042059														
765	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed														
1330	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	genbank 16s 49025 AB042058														
1328	T	A	A	T	C	G	C	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	G	C	Clostridium elmenteitii														
1354	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	Geobacillus subterraneus 16S AF276307														
1332	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	Sulfobacillus disulfidooxidans 16S U349														
1345	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	Bacillus thermoleovorans ribosomal RNA														
C G T T C C C G G G C C C T T G T A C A C A C C G C C C G T C																										Consensus #1																			
. . T . C C C																										Consensus #1																			
C G T T C C C G G G C C C T T G T A C A C A C C G C C C G T C																										Majority																			
1420													1430													1440																			
1363	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	43030 16s																
1363	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	genbank 16s 43030 AB059664																
1361	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	49029 16s																
1361	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	genbank 16s 49029 AB042059																
765	-	-	T	C	C	C	C	C	C	N																					cc-4902516SRDNA-t7p_C02_006-1-ed														
1360	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	genbank 16s 49025 AB042058																
1358	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	Clostridium elmenteitii																
1384	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	Geobacillus subterraneus 16S AF276307																
1362	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	Sulfobacillus disulfidooxidans 16S U349																
1375	C	G	T	T	C	C	G	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	C	Bacillus thermoleovorans ribosomal RNA																

Alignment 2

A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										Consensus #1
.										Consensus #1
A C A C C A C G A G A G T C G G G C A A C A C C C G A A G T C										Majority
1450										1470
1393	A	C	A	C	C	A	C	G	A	43030 16s
1393	A	C	A	C	C	A	C	G	A	genbank 16s 43030 AB059664
1391	A	C	A	C	C	A	C	G	A	49029 16s
1391	A	C	A	C	C	A	C	G	A	genbank 16s 49029 AB042059
770										cc-4902516SRDNA-t7p_C02_006-1-ed
1390	A	C	A	C	C	A	C	G	A	genbank 16s 49025 AB042058
1388	A	C	A	C	C	A	C	G	A	Clostridium elmenteitii
1414	A	C	A	C	C	A	C	G	A	Geobacillus subterraneus 16S AF276307
1392	A	C	A	C	C	A	C	G	A	Sulfobacillus disulfidooxidans 16S U349
1405	A	C	A	C	C	A	C	G	A	Bacillus thermoleovorans ribosomal RNA
G G T G . G G T A A C C C . T . . . G G G . G C C A G C C G										Consensus #1
.										Consensus #1
G G T G A G G T A A C C C G T G T A G G G A G C C A G C C G										Majority
1480										1500
1423	G	G	T	G	A	G	G	T	A	43030 16s
1423	G	G	T	G	A	G	G	T	A	genbank 16s 43030 AB059664
1421	G	G	T	G	A	G	G	T	A	49029 16s
1421	G	G	T	G	A	G	G	T	A	genbank 16s 49029 AB042059
770										cc-4902516SRDNA-t7p_C02_006-1-ed
1420	G	G	T	G	A	G	G	T	A	genbank 16s 49025 AB042058
1418	C	G	T	A	C	C	G	A	C	Clostridium elmenteitii
1444	G	G	T	G	A	G	G	T	A	Geobacillus subterraneus 16S AF276307
1422	G	G	T	G	A	G	G	T	A	Sulfobacillus disulfidooxidans 16S U349
1428										Bacillus thermoleovorans ribosomal RNA

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

	C	C	G	A	A	G	G	T	G	G	G	.	.	G	A	T	G	A	T	G	G	G	T	G	A	A	G	Consensus #1	
	Consensus #1
	C	C	G	A	A	G	G	T	G	G	G	T	C	G	A	T	G	A	T	G	G	G	T	G	A	A	G	Majority	

1510
1520
1530

1453	C	C	G	A	A	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G
1453	C	C	G	A	A	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G
1450	C	C	G	A	A	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G
1450	C	C	G	A	A	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G

43030 16s
genbank 16s 43030 AB059664
49029 16s
genbank 16s 49029 AB042059
CC-4902516SSPDNA-t7n C02 00

770

1448 C C G A A G G T G G G G T T G A T G A T T G G G G T G A A G
1445 T C G A A G G T G A A C C G A T A C T G G G G T G A A G
1473 C C G A A G G T G G G G C A A G T G A T T G G G G T G A A G
1451 C C G A A G G T G G G G C C G A T G A T T G G G G T G A A G

1428

T	C	G	T	A	A	C	A	G	G	T	A	G	C	C	G	T
.
T	C	G	T	A	A	C	A	G	G	T	A	G	C	C	G	T	X	X	X	X	X	X	X	X	X	X	X	X	X

Consensus #1
Consensus #1
Majority

1540 1550 1560

1483	T C G T A A C A A G G T A G C C G T	43030 16s
1483	T C G T A A C A A G G T A G C C G T	genbank 16s 43030 AB059664
1480	T C G T A A C A A G G T A G C C G T	49029 16s
1480	T C G T A A C A A G G T A G C C G T	genbank 16s 49029 AB042059

CC-4902516SPDNA-472 C02 00

770

1478	T C G G T A A C A A G G T A G C C G T A T C G G A A G G T G C
1475	T C G G T A A C A A G G T A T C C G T
1503	T C G G T A A C A A G G T A G C C G T A C C G G A A G G T G C
1481	T C G G T A A C A A G G T A G C C

1428

Alignment 2

.
.
X X X X X X X X X X X X X X

Consensus #1
Consensus #1
Majority

1570

1500

1513 G G T T G G A T

1497

1510 G G T T G G A T

770

1508 G G T T G G A

1492

1533 G G C T G G A T C A C C T C C T

1496

1428

43030 16S

genbank 16S 43030 AB059664

49029 16S

genbank 16S 49029 AB042059

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genbank 16S 49025 AB042058

Clostridium elmentei

Geobacillus subterraneus 16S AF276307

Sulfolobus solfataricus 16S U349

Bacillus thermoleovorans ribosomal RNA

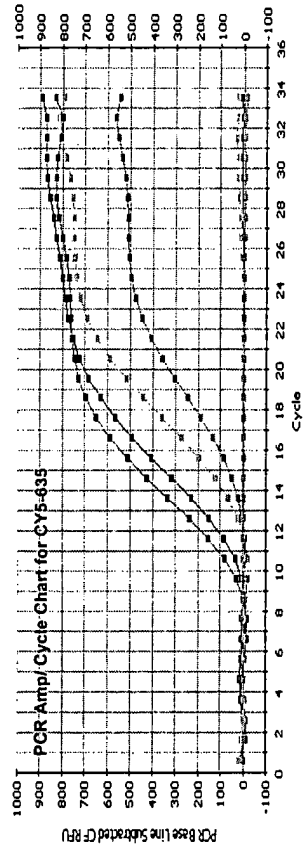
Consensus 'Consensus #1': When 60% (6) match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named 'Consensus #1' exactly.

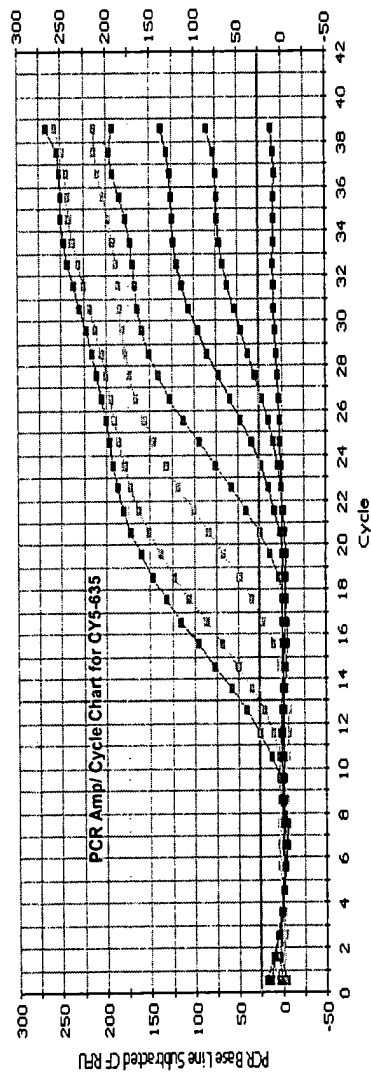
Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 9

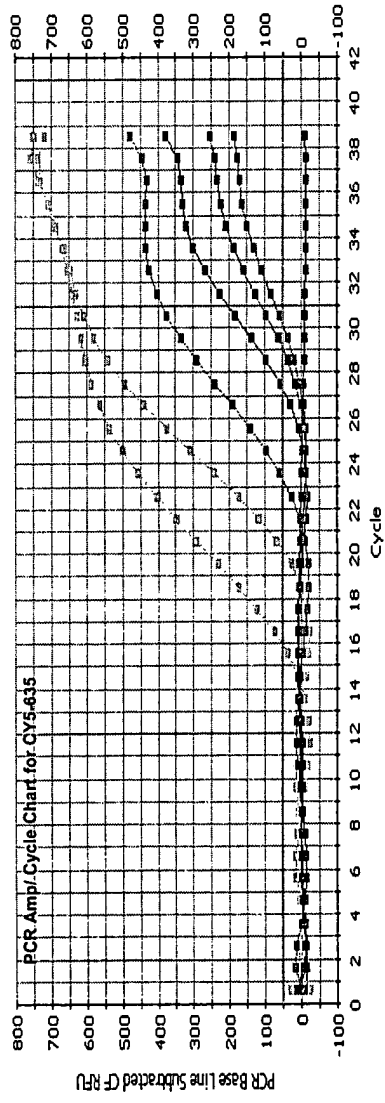


In addition, *G. stearothermophilus* can be seen in green. Other curves below the base line include the blank control (red) and the tests for *Lactococcus lactis* C2 (in blue), *P. putida* 49L/51 (purple) and *E. coli* DH5α (orange) using the same primer and probe set.

Figure 10



. Dilutions 10^0 (red), 10^{-1} (orange), 10^{-2} (light blue), 10^{-3} (purple), 10^{-4} (black), and 10^{-5} (blue) can be seen above the baseline. The blank control (brown) is below the baseline.



Dilutions 10^{-1} (orange), 10^{-2} (light blue), 10^{-3} (purple), 10^{-4} (black), 10^{-5} (blue) and 10^{-6} (green) can be seen above the baseline. The blank control (red) is below the baseline.

Figure 11

Figure 12

Zygosaccaromyces
 5 ATTGGCCCTCTANAGCATGCTCGACGGCCGCAGTGTGATGGATATCTGCAGAAATTCGGCTTTGCATGGCCGTTCTTAG
 TTGGTGGAGTGATTTGTCTGTCTTAATTGCCGATAACGAACGAGACCTTAACCTACTAAATAGTGGTGTAGCATTTGCTGG
 TTTTTCCACNTTCTTAGAGGGACTATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGA
 CGTTCTGGGCCCGCACGGCGCTACACTGACGGAGCCAGCGAGTCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAA
 CTCCGTCTGTGGGATAGAGCATTTGTAATTATTGCTCTTCAACGAGGAATTCCCTAGTAAGCGCAAGTCATCAACTTGC
 10 GTTGATTACGTCCCTGCCCTTTGTACACACAAGCCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGG
 TACCAAGCTTGGCGTAATCATGGTCATAGCTGTGTTCTCTGTGTGAAAATTGTTATCCGCTCACAAATCCACACAACATACGA
 GCCGGAAGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCCGC
 TTTCCAGTCGGGAAACCTGTCTGTGCCAGCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGCGTATTGGGC
 GCTCTTCCGCTTCCCTCGCTCACTGACTCGCTCGGTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGG
 GTAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCANANGCCAGGANCCTGT
 15 AAAGGCCGCGTGTGGCGTTTTCNCNTANGCTCGCCCCCTGACAGCATNCAAAAATCGACGCTCAGTCNNANGTGGCGAAC
 CCGNNGGANATAAGATACNNGCGTTNCCCCGTGNANCTCCNCNTGGCTNTCNGNTCNANCNCGNCGNTANGGAANCTGNCNC
 CTTCNCCTTNGGAACNGGNNCTTNNNNNNNANCNNGNNNNNNNNNNNGGNNN

Figure 13

Penicillium digitatum

```
5  GANGNCNNCCNNANNTNNATCCCTNAGCNGAGTNGNNAAGGCNCGTTNCCGANGGAGAAGNGGACAGGTNTCCGTANCGC
   AGGTNNGANCAGGAGAGCGCACGAGGGAGCTNCAGGGGGAACGCCCTGGGATCTTNATAGTCCNGTCGGGTTTCNCCACNT
   CTGACTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCNTATGGAAAACGCCAGCAACCGGGCCCTTTTACGGTT
   CCTGGCNTTTGTGGCCCTTTTGCTCACATGTTCTTCCCTGCCGTTATCCCCCTGATTCTGTGGATAACCGTATTACCGCCTT
   TGAGTGAGCTGATACCGCTCGCCGCGAGCCGAAACGACCGAGCGAGTCAGTGAGCGGAGGAAGCGGAAAGCGGCCCAA
   10  TACGCAAAACCGCCTCTCCCCGCGGTTGGCCGATTCAATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAAGCGGGC
   AGTGAGCGCAACGCAATTAAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTAT
   GTTGTGTGGAAATTGTGAGCGGATAACAAATTTCAACAGGAAACAGCTATGACCATGATTACGCCAAAGCTTGGTACCGAGC
   TCGGATCCACTAGTAACGGCCGCGCAGTGTGCTGGAAATTCGGCTTTGCATGGCCGTTCTTAGTTGGTGAGTGATTGTCT
   15  GCTTAAATTGCGATAACGAACGAGACCTCGGCCCTTAAATAGCCCGTCCGCATTTGCGGGCCGCTGGCTTCTTAAGGGGA
   CTATCGGCTCAAGCCGATGGAAAGTGCGCGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCCGACCGCGGCTA
   CACTGACAGGGCCAGCGAGTACATCACCTTAACGAGAGGTTTGGGTAATCTTGTAAACCTGTGCTGCTGGGATAGA
   GCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAGGCACGAGTCAATCAGCTCGTGCCGATTACGTCCCTGCCCCTT
   TGTACACACAAGCCGAATTCTGCAGATAATCCATCACACTGGCGGCCGTCGAGCATGCTNTAGAGGGCCCAAT
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5 10 15

Figure 15

PCR Amp/Cycle Graph for FAM-490

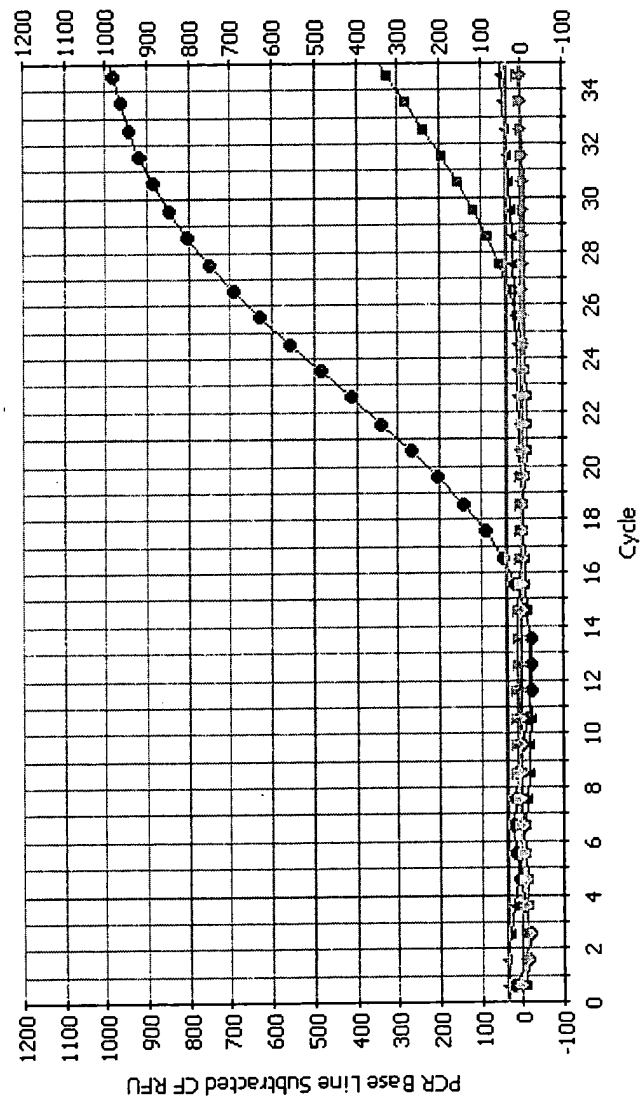


Figure 16

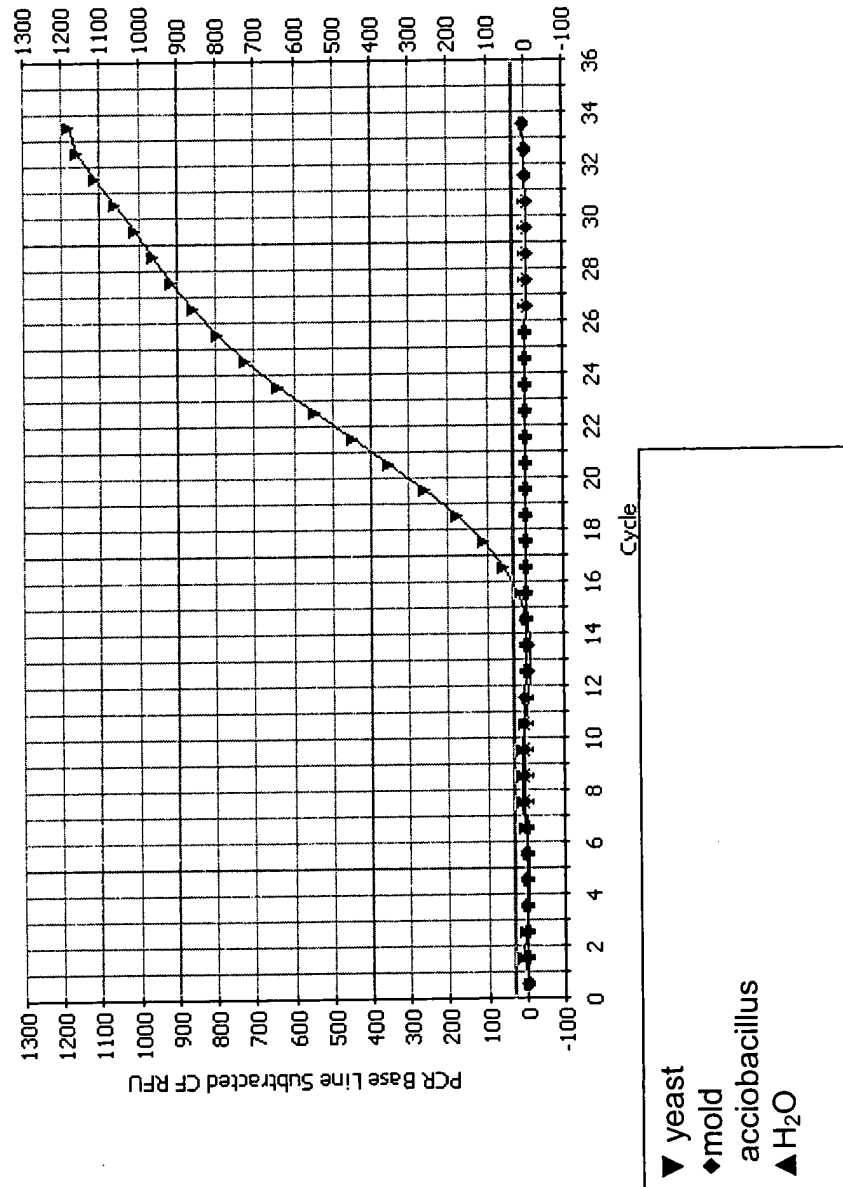
PCR Amp/Cycle Graph for FAM-490

Figure 17

PCR Amp/Cycle Graph for FAM-490

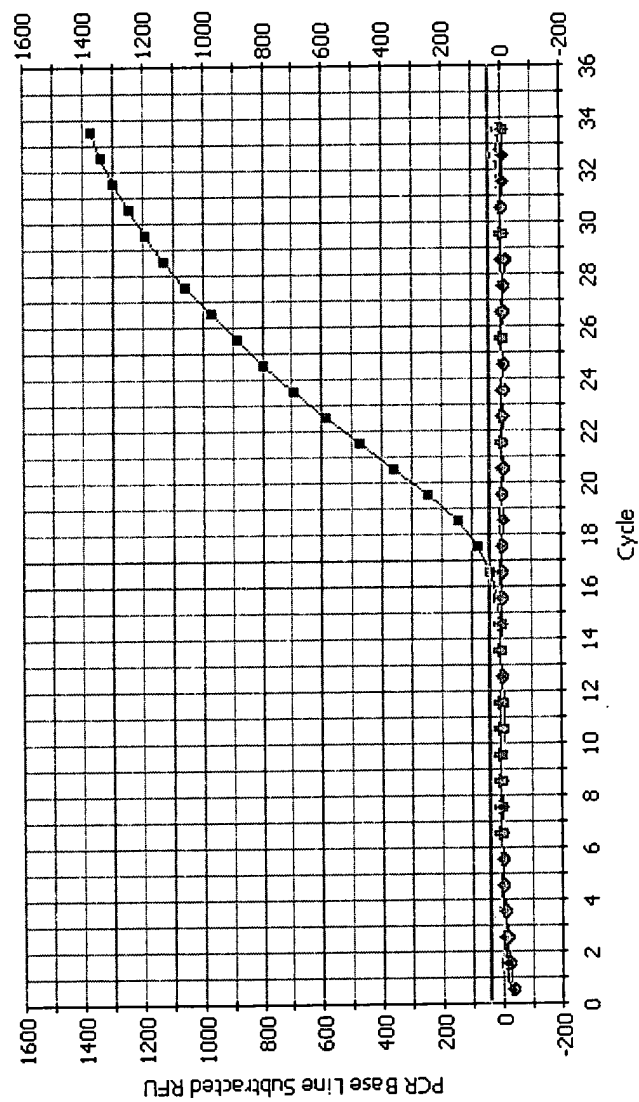


Figure 18

PCR Amp/Cycle Graph for FAM-490

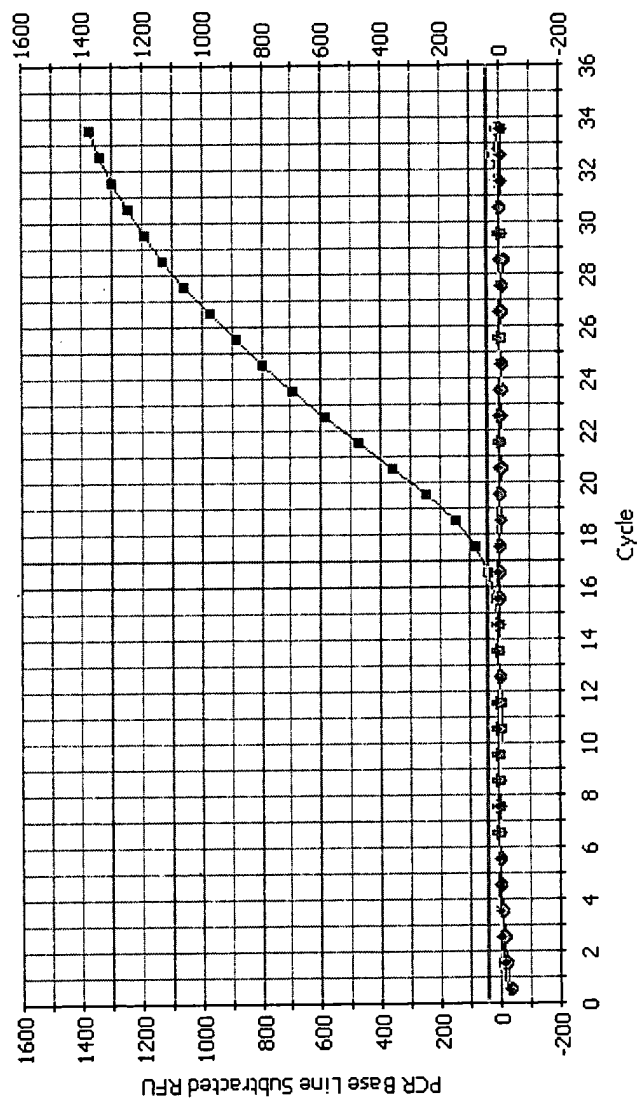
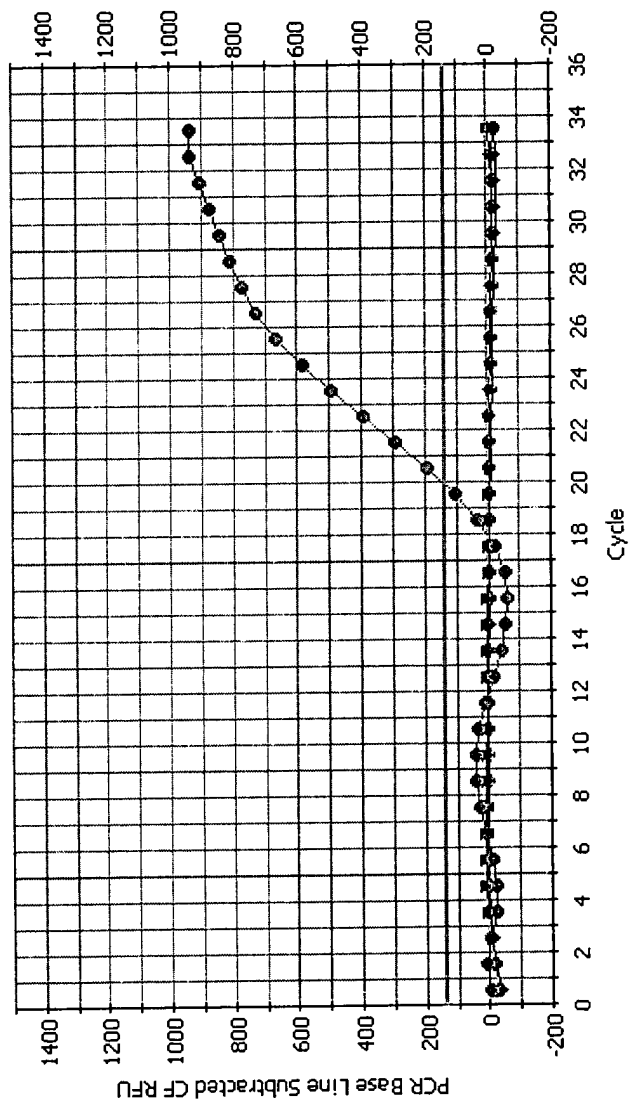


Figure 19

PCR Amp/Cycle Graph for FAM-490



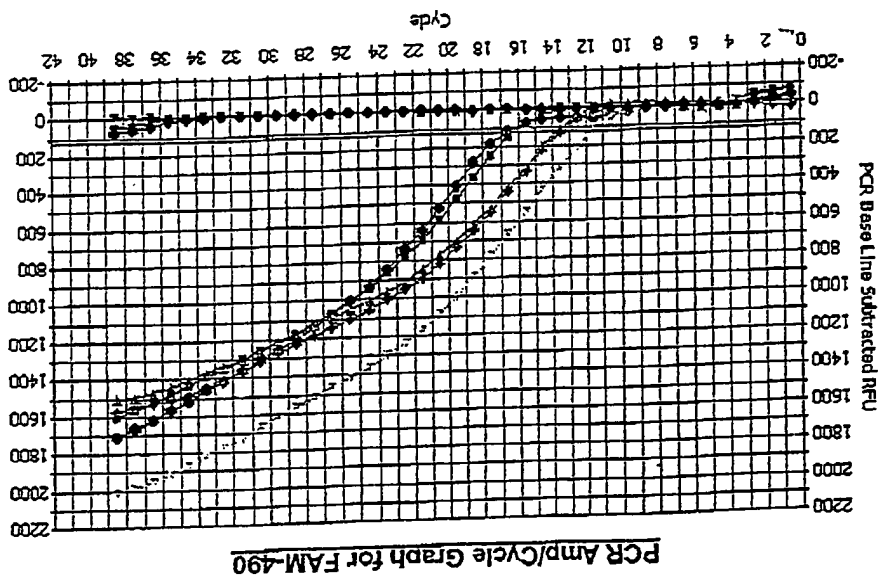


Figure 20

Figure 21

PCR Amp/Cycle Graph for FAM-490

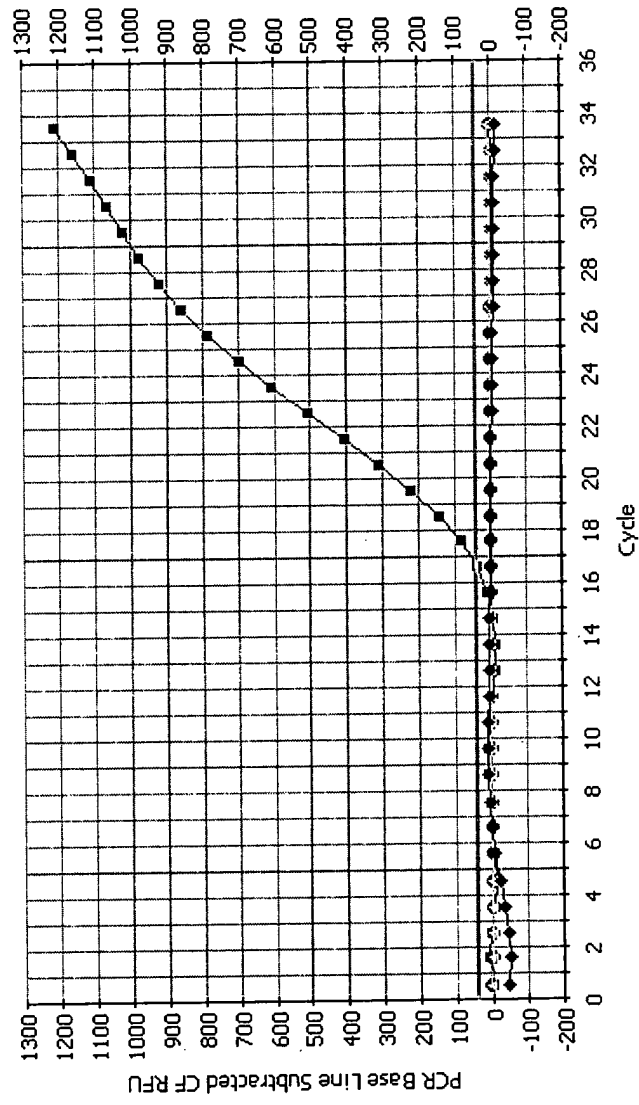


Figure 22

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1  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
2  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
3  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
4  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
5  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
6  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
7  CCCAGTTTCGGATTGAGGGCTTGCAACTCGCCCCCATGAAGT
8  CTCAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
9  CGTAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
10 CTCAGTTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC

1  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT
2  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT
3  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
4  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
5  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
6  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
7  TGGAGTTGCTAGTAATCGCGAATCAGCATGTCGCGGTGAATGCGTTT
8  CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT
9  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
10 CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT

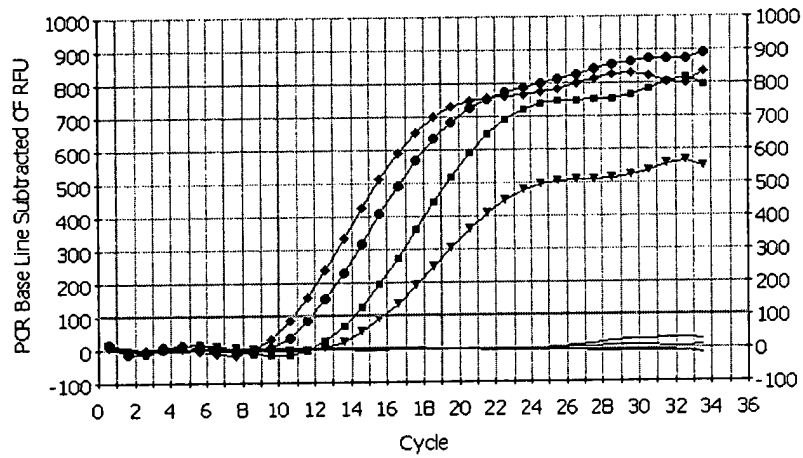
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2  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
3  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
4  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
5  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
6  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
7  CCGGGTCTTGTACACACCGCCCGTCACACACCGGAAGTTCGGAAGCAC
8  CCGGGCCTTGTACACACCGCCCGTCACACACGAGAGCTTGCAACAC
9  CCGGGCCTTGTACACACCGCCCGTCACACACGAGAGTTCGCAACAC
10 CCGGGCCTTGTACACACCGCCCGTCACACACGAGAGCTCGCAACAC

```

^a 16S rDNA Sequences in the alignment are 16S rDNA sequences from the following organisms (GenBank accession numbers follow if applicable): 1) *A. acidocaldarius* strain ATCC 43030, 2) *A. acidocaldarius* strain DSM 454 (AB059664), 3) *A. cycloheptanicus* strain ATCC 49029, 4) *A. cycloheptanicus* strain DSM 4006 (AB042059), 5) *A. acidoterrestris* strain ATCC 49025, 6) *A. acidoterrestris* strain DSM 3923 (AB042058), 7) *Clostridium elmenteitii* isolate E2SE1-B (AJ271453), 8) *Geobacillus subterraneus* strain K (AF276307), 9) *Sulfobacillus disulfidooxidans* SD-11 (U34974), and 10) *B. thermoleovorans* strain ATCC 43513 (M77488) ^b

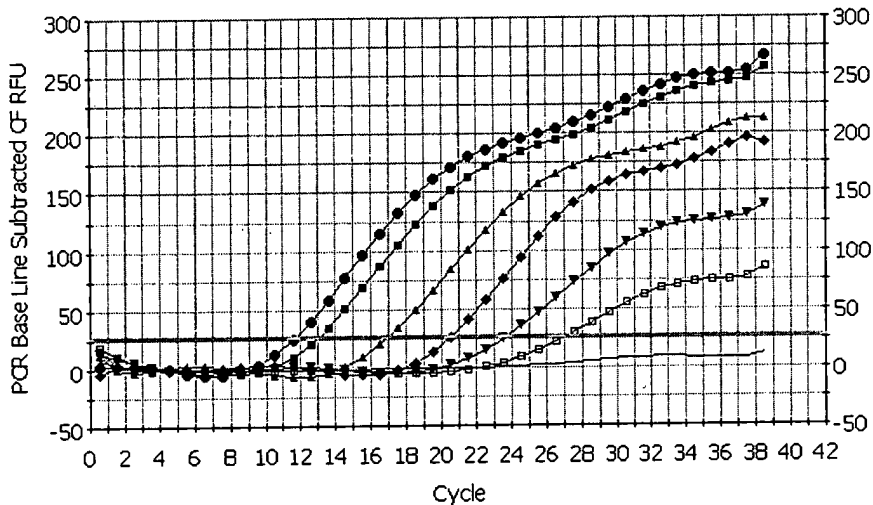
Note CC16S-R is in 5' to 3' orientation in alignment. Actual primer sequence is the reverse complement.

Figure 23



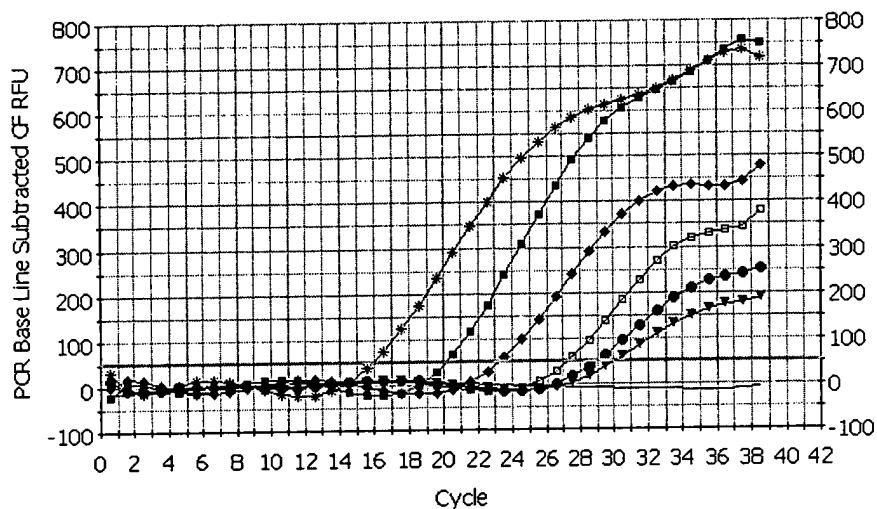
In addition, *G. stearo**thermophilus* ATCC 10149 (▼) can be detected. Curves below the base
5 line include the blank control, *Lactococcus lactis* C2, *P. putida* 49L/51, and *E. coli* DH5 α . This
is a representative curve of repeated trials.

Figure 24



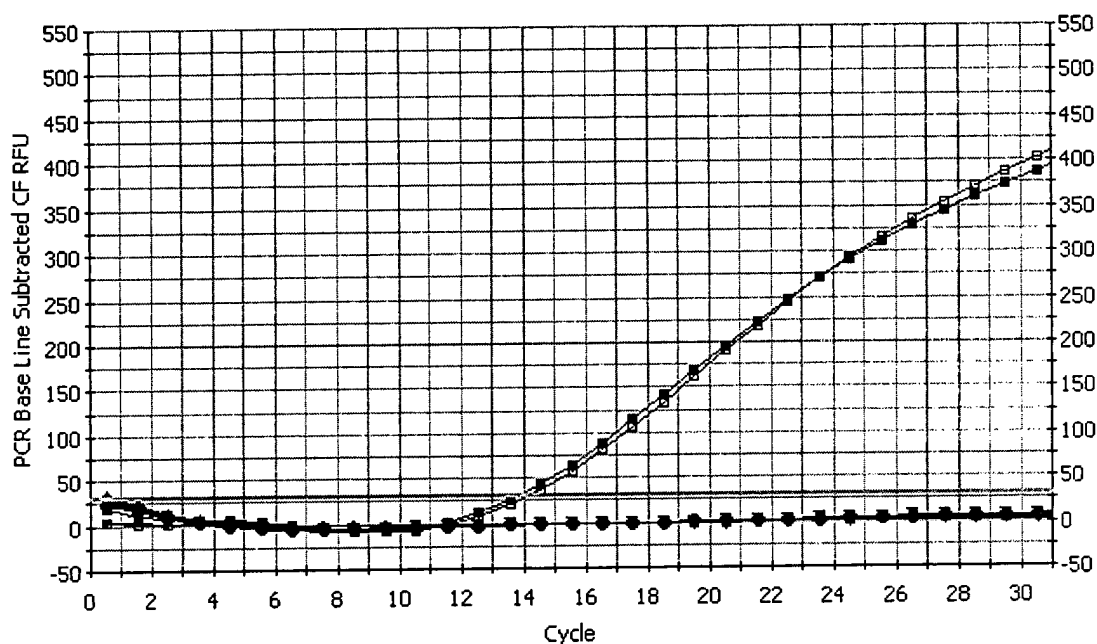
. Ten-fold serial dilutions were performed, and cell numbers^a represented at each curve are as follows: 1.6x10⁷ CFU/ml (●), 1.6x10⁶ CFU/ml (■), 1.6x10⁵ CFU/ml (▲), 1.6x10⁴ CFU/ml (◆), 1.6x10³ CFU/ml (▼), and 1.6x10² CFU/ml (□) appear above the baseline. The water control is below the baseline. This is a representative curve of repeated trials. ^a Cell numbers were calculated by finding the CFU/ml of plated samples and multiplying by the dilution level of the representative curve.

Figure 25



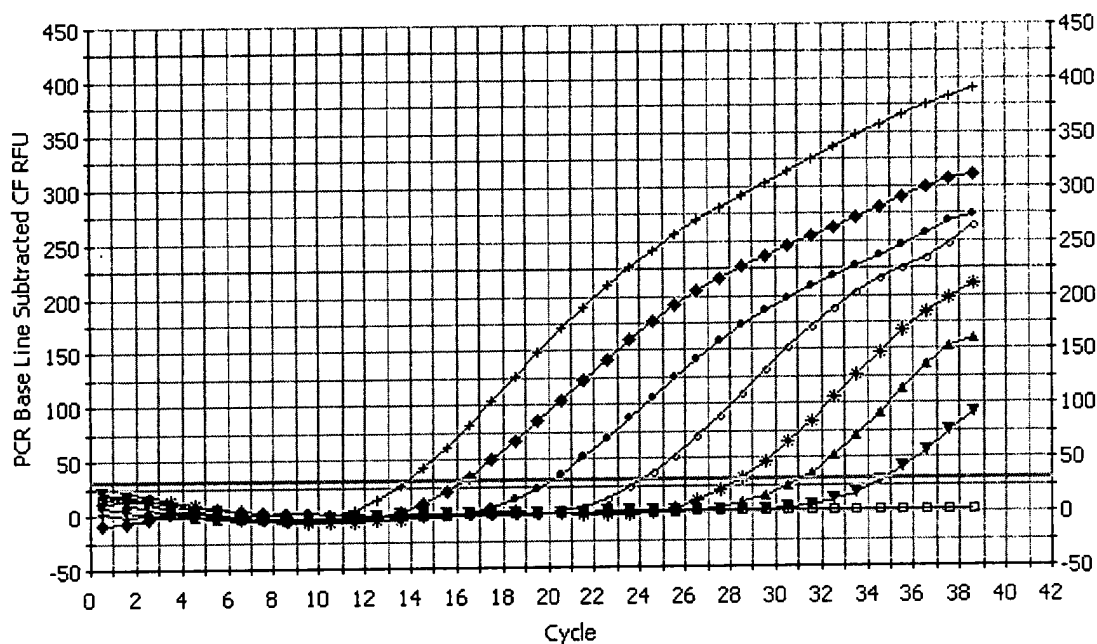
- 5 Cell counts at each curve are as follows: 6.3×10^6 CFU/ml (*), 6.3×10^5 CFU/ml (■), 6.3×10^4 CFU/ml (◆), 6.3×10^3 CFU/ml (□), 6.3×10^2 CFU/ml (●), and 6.3×10^1 CFU/ml (▼) appear above the baseline. The water control is below the baseline. This is a representative curve of repeated trials.

Figure 26



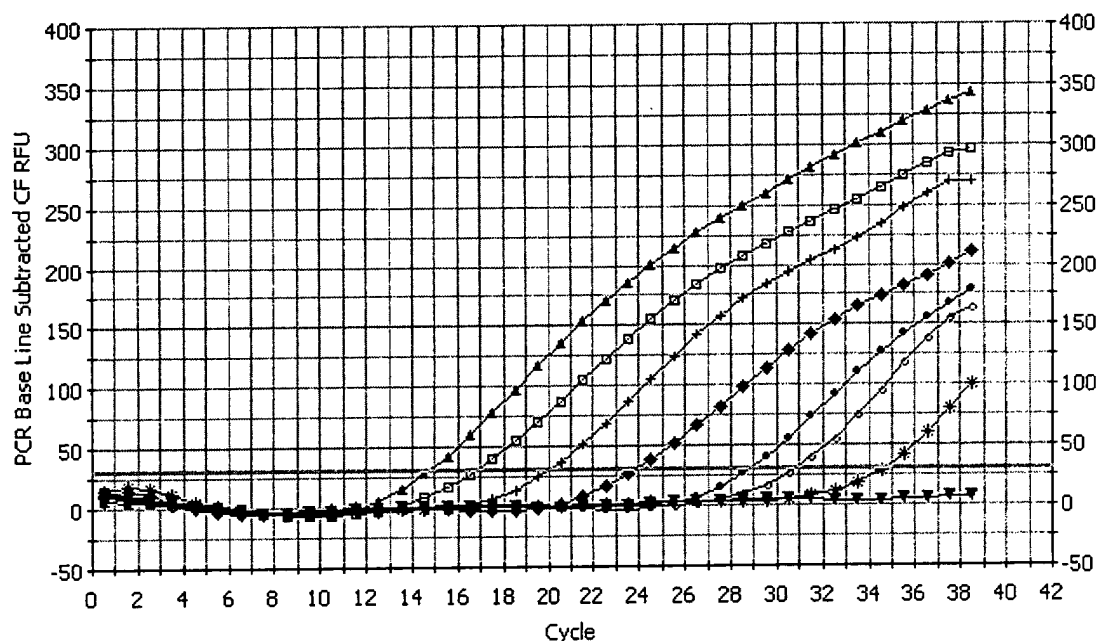
- 5 *A. acidoterrestris* ATCC 49025 (■) , *A. acidocaldarius* ATCC 43030 (□), 6 other bacteria under the detection baseline: *Bacillus subtilis* OSU 456, *Pseudomonas putida* 49L/51, *E. coli* DH5α , *Listeria monocytogenes* V7, *Lactococcus lactis* ML3 and *Geobacillus* ATCC 10149 ■ *Alicyclobacillus acidoterrestris* ATCC49025 ; □ *Alicyclobacillus acidocaldarius* ATCC43030; + *Bacillus subtilis* OSU456; ● *E. coli* DH5α; ▲ *Pseudomonas putida* 49L/51; ▼ *Geobacillus* ATCC 10149; ♦ *Lactococcus lactis* ML3 ; ○ *Listeria monocytogenes* V7

Figure 27



- 5 ▲ 1ml saline with 4×10^6 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml saline with 4×10^5 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- + 1ml saline with 4×10^4 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ◆ 1ml saline with 4×10^3 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml saline with 4×10^2 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 10 ○ 1ml saline with 4×10^1 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- * 1ml saline with 4CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ▼ 1ml saline

Figure 28



5

- ◆: 10^6 cells; ▤: 10^4 cells; ▼: 10^2 cells; ●: bacterial medium (blank) control.
- ▲ 1ml apple juice with 4×10^6 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml apple juice with 4×10^5 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- + 1ml apple juice with 4×10^4 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ◆ 1ml apple juice with 4×10^3 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml apple juice with 4×10^2 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml apple juice with 4×10^1 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- * 1ml apple juice with 4CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

15 ▼ 1ml apple Juice